

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: GAMDEL Examiner #: 70675 Date: 7/19/01
 Art Unit: 1644 Phone Number 308 3997 Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle) PAPER DISK E-MAIL

1644 MILBOY 9012
 If more than one search is submitted, please prioritize searches in order of need. 8803

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: OB/487203

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

SEQ + SEQ INTERVIEW IS SCHEDULED

- ① SEQ ID NO: 8 NA
- ② SEQ ID NO: 8 NA
- ③ SEQ ID NO: 12 NA
- ④ SEQ ID NO: 12 (1-12 NA)
- ⑤ 8-12 OF SEQ ID NO: 1 CLOSED
- ⑥ SEQ ID NO: 1 CLOSED

FRANK REQUEST JRU

STAFF USE ONLY

Searcher: Jan
 Searcher Phone #: 4498
 Searcher Location: _____
 Date Searcher Picked Up: 7/19
 Date Completed: 7/20/01
 Searcher Prep & Review Time: _____
 Clerical Prep Time: 30
 Online Time: 45

Type of Search

NA Sequence (#) 2
 AA Sequence (#) 4
 Structure (#) _____
 Bibliographic _____
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Questel/Orbit _____
 Dr. Link _____
 Lexis/Nexis _____
 Sequence Systems ✓
 WWW/Internet _____
 Other (specify) _____


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OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE
RC STRAIN=AF-285;
RA Sarma P.O., Gupta T.M., Fairwell T.;
RL Submitted (DEC-1999) to the SWISS-PROT data bank.
CC -!- FUNCTION: BINDS TO IGG AND IGE.
KW Allergen; IgE-binding protein; IgG-binding protein.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2290 MW; 46D1CEB3AB2BF585 CRC64;

Query Match 27.1%; Score 29; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGKSS 10
Db 12 QGKSS 17

RESULT 3
Q9R4D2 PRELIMINARY; PRT; 20 AA.
ID Q9R4D2
AC Q9R4D2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE 40.5 KDA IGA NEPHROPATHY-ASSOCIATED OUTER MEMBRANE ANTIGEN (FRAGMENT).
OS Haemophilus parainfluenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=729;
RN [1]
RP SEQUENCE.
RX MEDLINE=96215401; PubMed=8625525;
RA Suzuki S., Nakatomi Y., Odani S., Sato H., Geijo F., Arakawa M.;
RT "Circulating IGA, IgG, and IgM class antibody against Haemophilus
RT parainfluenzae antigens in patients with Iga nephropathy.";
RL Clin. Exp. Immunol. 104:306-311(1996).
SQ SEQUENCE 20 AA; 2153 MW; 4CD523E74E5639E5 CRC64;

Query Match 26.2%; Score 28; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIDHQGK 8
Db 3 VIDNEGK 10

RESULT 4
Q9QVA2 PRELIMINARY; PRT; 17 AA.
ID Q9QVA2
AC Q9QVA2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PROTEIN KINASE C SUBSTRATE PP80 (FRAGMENT).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=93099617; PubMed=1464108;
RA Komatsu S., Hirano H.;
RT "80 kDa mouse sperm protein as a substrate of protein kinase C.";
RL Chem. Pharm. Bull. 40:2780-2782(1992).

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SQ SEQUENCE 17 AA; 2025 MW; B8272D8940BD0B41 CRC64;

Query Match 23.4%; Score 25; DB 11; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 KSKKCVQRKVEG 19
Db 4 KSEKVVFKXLEG 15

RESULT 5
Q40499 PRELIMINARY; PRT; 18 AA.
ID Q40499
AC Q40499;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ELONGATION FACTOR 1-A (FRAGMENT).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=19;
RX MEDLINE=94035181; PubMed=8220482;
RA Marty I., Brugidou C., Chartier Y.;
RT "Growth-related gene expression in Nicotiana tabacum mesophyll
RT protoplasts.";
RL Plant J. 4:265-278(1993).
DR EMBL; Z14080; CAA78458.1; -
KW Elongation factor.
SQ NON_TER 1
SQ SEQUENCE 18 AA; 1983 MW; 5FB7282474069C97 CRC64;

Query Match 23.4%; Score 25; DB 10; Length 18;
Best Local Similarity 35.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 DHQGTKSSKCVROK 16
Db 3 DPTGAKVTRAAQKK 16

RESULT 6
O93044 PRELIMINARY; PRT; 21 AA.
ID O93044
AC O93044;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE 17.6 KDA REPB PROTEIN (FRAGMENT).
GN REPB.
OS Maize streak virus.
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
OX NCBI_TaxID=10821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP1 FROM REUNION ISLAND;
RX MEDLINE=97049057; PubMed=8893787;
RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
RT "Infectivity and complete nucleotide sequence of the genome of a
RT genetically distinct strain of maize streak virus from Reunion
RT Island.";
RL Arch. Virol. 141:1637-1650(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP1 FROM REUNION ISLAND;
RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;

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"Onaspecies nature of three related maize streak virus isolates
 RT obtained through different mode of selection."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ224499; CAA12284.1;
 FT NON_TER 21
 SO SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 23.4%; Score 25; DB 14; Length 21;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 12 CVRQVSGS 20
 I:: III
 DB 5 CIOSSDEGS 13

RESULT 7
 093046 PRELIMINARY; PRT; 21 AA.
 AC 093046;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DE 01-NOV-1998 (TREMBlrel. 08, last annotation update)
 DE 17.6 KDA REPB PROTEIN (FRAGMENT).
 GN REPB.
 OS Maize streak virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=10821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPI FROM REUNION ISLAND;
 RA MEDLINE-97049057; PubMed-8893787;
 RA Peterschmitt M., Granier M., Frutos R., Reynaud B.,
 RT "Infectivity and complete nucleotide sequence of the genome of a
 RT genetically distinct strain of maize streak virus from Reunion
 RT Island.";
 RL Arch. Virol. 141:1637-1650(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPI FROM REUNION ISLAND;
 RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
 RT "Quaspecies nature of three related maize streak virus isolates
 RT obtained through different mode of selection."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ225000; CAA12287.1;
 FT NON_TER 21
 SO SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 23.4%; Score 25; DB 14; Length 21;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 12 CVRQVSGS 20
 I:: III
 DB 5 CIOSSDEGS 13

RESULT 8
 093047 PRELIMINARY; PRT; 21 AA.
 AC 093047;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DE 01-NOV-1998 (TREMBlrel. 08, last annotation update)
 DE 17.6 KDA REPB PROTEIN (FRAGMENT).
 GN REPB.
 OS Maize streak virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=10821;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-SPI FROM REUNION ISLAND;
 RX MEDLINE-97049057; PubMed-8893787;
 RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
 RT "Infectivity and complete nucleotide sequence of the genome of a
 RT genetically distinct strain of maize streak virus from Reunion
 RT Island.";
 RL Arch. Virol. 141:1637-1650(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPI FROM REUNION ISLAND;
 RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
 RT "Quaspecies nature of three related maize streak virus isolates
 RT obtained through different mode of selection."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ225001; CAA12290.1;
 FT NON_TER 21
 SO SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 23.4%; Score 25; DB 14; Length 21;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 12 CVRQVSGS 20
 I:: III
 DB 5 CIOSSDEGS 13

RESULT 9
 075729 PRELIMINARY; PRT; 12 AA.
 AC 075729;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, last annotation update)
 DE NEF (NEF).
 GN NEF.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H94FL;
 RA Mariani R., Kirchhoff F., Greenough T.C., Sullivan J.L.,
 RA Desrosiers R.C., Skowronski J.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U61801; AAB04720.1;
 DR InterPro: IPR000583;
 DR PROSITE: PS00443; GATASE_TYPE_II; UNKNOWN_1.
 DR PROSITE: PS00443; GATASE_TYPE_II; UNKNOWN_1.
 SO SEQUENCE 12 AA; 1238 MW; 2B921E1187B325A3 CRC64;

Query Match 22.4%; Score 24; DB 14; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.8e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GTRSSKC 12
 I:: III
 DB 2 GTRSSKC 8

RESULT 10
 09WT8 PRELIMINARY; PRT; 18 AA.
 ID 09WT8;
 AC 09WT8;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
 DE 01-NOV-1999 (TREMBlrel. 12, last annotation update)
 DE R-RAS GTPASE ACTIVATING PROTEIN (FRAGMENT).
 GN R-RAS GAP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.


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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAQUE-DAWLEY;
RA Iwashita S., Kobayashi M.;
RT "NGF-mediated downregulation of R-ras GAP expression.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020479; BAA78368.1; -
FT NON_TER 18
SQ SEQUENCE 18 AA; 2104 MW; 6BC3355FDC91E28A CRC64;

Query Match 22.4%; Score 24; DB 11; Length 18;
Best Local Similarity 25.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 IDHQGTSSKCVROKV 17
Db : : : : :
3 VEEGLRVFOSVRIKI 18

RESULT 11
Q9TRQ5 PRELIMINARY; PRT; 19 AA.
AC Q9TRQ5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CALCULIN-ASSOCIATED PROTEIN PEPTIDE L-II, CAP-50-ANNEXIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92317074; PubMed=1618851;
RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RA Kobayashi R., Hidaka H.;
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
RT fibroblast 3Y1 cells.";
RL J. Biol. Chem. 267:13498-13504(1992).
SQ SEQUENCE 19 AA; 2144 MW; F3994AFD0DE7CB05 CRC64;

Query Match 22.4%; Score 24; DB 6; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.7e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 6 GTKSSKCVROKV 17
Db : : : : :
6 GTKDXLRDQV 17

RESULT 12
Q93050 PRELIMINARY; PRT; 21 AA.
AC Q93050;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE 17.6 KDA REP PROTEIN (FRAGMENT).
GN REPB.
OS Maize streak virus.
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
OX NCBI_TaxID=10821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SP2 FROM REUNION ISLAND;
RX MEDLINE=97049057; PubMed=8893787;
RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
RT "Infectivity and complete nucleotide sequence of the genome of a
RT genetically distinct strain of maize streak virus from Reunion
Island.";
RL Arch. Virol. 141:1637-1650(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SP2 FROM REUNION ISLAND;
RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
RT "Quasiespecies nature of three related maize streak virus isolates
RT obtained through different mode of selection.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225005; CAA12297.1; -
FT NON_TER 21
SQ SEQUENCE 21 AA; 2378 MW; 267B619FB848A32B CRC64;

Query Match 22.4%; Score 24; DB 14; Length 21;
Best Local Similarity 44.4%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 CVRKQVEGS 20
Db : : : : :
5 CIQTSDEGS 13

RESULT 13
Q9QVD5 PRELIMINARY; PRT; 13 AA.
AC Q9QVD5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
RT cytosol.";
RL J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 13 AA; 1537 MW; 3EA2F724AD8B85B8 CRC64;

Query Match 22.0%; Score 23.5; DB 11; Length 13;
Best Local Similarity 37.5%; Pred. No. 2.3e+03;
Matches 6; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 1 VIDHQGTSSKCVROK 16
Db : : : : :
1 ITHHSGMDQ---RQK 13

RESULT 14
Q9SQI6 PRELIMINARY; PRT; 15 AA.
AC Q9SQI6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TRANSLATION ELONGATION FACTOR (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
OC Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Z.-Y., Chen S.-Y.;
RT "Inducible expression of translation elongation factor 1A gene in rice
RT seedlings in response to environmental stresses.";
```

RL Act² Bot. Sin. 41:800-806(1999).
 DR EMBL; AF067195; AAC79991.1; -;
 DR InterPro; IPR001153; -;
 DR ProDom; PD004535; -; 1.
 KW Elongation factor.
 FT NON_TER 1
 SO SEQUENCE 15 AA; 1514 MW; 95E5C46F069C9775 CRC64;

Query Match 21.5%; Score 23; DB 10; Length 15;
 Best Local Similarity 35.7%; Pred. No. 3.2e+03;
 Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 3 HQGTKSSKCVNRQK 16
 | | : | : |
 Db 1 DPTGAKVTAKAAKK 14

RESULT 15

O9LMD7 PRELIMINARY; PRT; 17 AA.
 AC O9LMD7;
 DT 01-OCT-2000 (TRENBLREL. 15, Created)
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
 DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
 DE F14D16.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 NX NCBI_TaxID=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RP Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bei Q., Chin C., Chou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F14D16 from chromosome
 I.",
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei Q., Chin C., Chou J., Choi E.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC068602; AAF79279.1; -;
 SO SEQUENCE 17 AA; 1987 MW; 518C4C484C814DE6 CRC64;

Query Match 21.5%; Score 23; DB 10; Length 17;
 Best Local Similarity 44.4%; Pred. No. 3.6e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 HQGTKSSK 12
 | : | : |
 Db 8 HHLSPSSRC 16

Search completed: July 19, 2001, 07:50:05
 Job time: 171 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:46:49 ; Search time 18 Seconds
(without alignments)
70.728 Million cell updates/sec

Title: US-08-487-283A-1
Perfect score: 107
Sequence: 1 VIDHOGTKSKKCVKQVEGSS 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 163282

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_0601:*

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2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	21	16	AA197605
2	36	33.6	19	21	AA552695
3	32	29.9	9	16	AA67862
4	32	29.9	9	16	AA68909
5	32	29.9	11	11	AA605852
6	32	29.9	11	16	AA67860
7	32	29.9	11	16	AA68908
8	32	29.9	14	20	AA68479
9	31	29.0	9	21	AA67659
10	31	29.0	20	19	AA55855
11	31	29.0	20	19	AA55845

12	31	29.0	20	19	AA55848	HIV p17 gag protei
13	31	29.0	20	19	AA55851	HIV p17 gag protei
14	30	28.0	21	21	AA523773	Entry vector pENTR
15	29	27.1	13	14	AA535477	Phosphatidylserine
16	29	27.1	14	19	AA53864	Gravin polypeptide
17	29	27.1	14	21	AA515884	Human gravin poten
18	29	27.1	15	21	AA779915	Rhesus monkey papl
19	29	27.1	15	21	AA501692	Nuclear localisati
20	28	26.2	15	10	AA90197	Antigenic peptide
21	28	26.2	15	21	AA65517	Oestrogen receptor
22	28	26.2	18	22	AA550505	CD40-binding pepti
23	28	26.2	20	16	AA68766	Cytotoxic T Lympho
24	28	26.2	20	17	AA99360	Beta-casein fragme
25	28	26.2	20	19	AA53854	HIV p17 gag protei
26	28	26.2	20	19	AA55856	HIV p17 gag protei
27	28	26.2	20	19	AA55858	HIV p17 gag protei
28	28	26.2	20	19	AA55859	HIV p17 gag protei
29	28	26.2	20	19	AA55860	HIV p17 gag protei
30	28	26.2	20	19	AA55861	HIV p17 gag protei
31	28	26.2	20	19	AA55843	HIV p17 gag protei
32	28	26.2	20	19	AA55846	HIV p17 gag protei
33	28	26.2	20	19	AA55847	HIV p17 gag protei
34	28	26.2	20	19	AA55849	HIV p17 gag protei
35	28	26.2	20	19	AA55850	HIV p17 gag protei
36	27.5	25.7	18	19	AA683057	Human Fas peptide
37	27.5	25.7	18	21	AA614765	Human Fas epitope,
38	27.5	25.7	18	21	AA690915	Human Fas extracel
39	27	25.2	10	3	AA920202	Sequence of peptid
40	27	25.2	10	3	AA920326	Decapeptide with t
41	27	25.2	11	3	AA920205	Sequence of peptid
42	27	25.2	11	22	AA572850	Human p53 S121C mu
43	27	25.2	12	19	AA686708	Synthetic peptide
44	27	25.2	13	3	AA920327	Tridecapeptide wit
45	27	25.2	14	20	AA901111	CTGF peptide fragm

ALIGNMENTS

RESULT 1		
ID	AA197605	standard; Protein: 21 AA.
AC	AA197605;	
XX		
DT	02-APR-1996	(first entry)
DE	Pro-C5 polypeptide KSSKC epitope.	
XX		
KW	Complement C5; haemolysis; kidney; glomerulonephritis;	
KM	monoclonal antibody; antiinflammatory; antibody engineering;	
KM	humanised antibody; KSSKC epitope.	
XX		
OS	Homo sapiens.	
PN	WO9529697-A1.	
XX		
PD	09-NOV-1995.	
XX		
PF	01-MAY-1995;	95WO-US05688.
XX		
PR	02-MAY-1994;	94US-0236208.
XX		
PA	(ALEX-) ALEXION PHARM INC.	
XX		
PI	Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;	
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;	
PI	Wang Y, Wilkins JA;	
XX		
DR	WPI; 1995-392923/50.	
XX		
PT	Treating glomerulonephritis with antibody against complement C5	
PT	component - to inhibit complement induced cell lysis	

XX Example 13; Page 81; 181pp; English.

XX The cDNA sequence of the complement C5 gene transcript predicts a

CC secreted pro-C5 precursor of 1676 amino acids (AAR77604). C5 is a

CC beta-globulin heterodimer thought to play a role in the pathogenesis

CC of glomerulonephritis (GN). Cleavage of the C5 alpha-chain

CC by a convertase enzyme generates anaphylatoxic C5a. Monoclonal

CC and humanised recombinant antibodies that recognise the alpha-chain

CC KSSKC epitope (AAR77605) block C5a generation, thereby reducing

CC glomerular inflammation and kidney dysfunction associated with GN.

XX Sequence 21 AA;

SQ

Query Match 100.0%; Score 107; DB 16; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VIDHGTGKSSKCVRKVEGSS 21

Db 1 vidhgtksskcvrkvegss 21

RESULT 2

AAV52695

ID AAV52695 standard; peptide; 19 AA.

XX

AC AAV52695;

XX

DT 07-MAR-2000 (first entry)

XX

DE Synthetic fibrinogen C-terminus peptide, peptide-07.

XX

KW Fibrinogen; C-terminus; cell adhesion; cell binding; proliferation;

KW wound healing; diabetes mellitus; clotting; coagulation; disorder;

KW haemophilia A; factor VIII deficiency; haemophilia B;

KW factor IX deficiency; cell culture; separation; cell transplantation;

KW therapeutic structure; research tool; diagnosis.

XX

OS Synthetic.

XX

PN WO9961041-A1.

XX

PD 02-DEC-1999.

XX

PF 26-MAY-1999; 99WO-US11517.

XX

PR 27-MAY-1998; 98US-0084371.

XX

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PA (VITE-) VI TECHNOLOGIES INC.

XX

PI Gorodetsky R, Marx G;

XX

DR WPI; 2000-062582/05.

XX

PT New peptides corresponding to fibrinogen carboxy terminus, used for

PT promoting wound healing -

XX

PS Example 1; Page 12; 46pp; English.

XX

CC This sequence represents a synthetic peptide, peptide-07, which

CC corresponds to a fibrinogen alpha chain C-terminal sequence.

CC However, unlike the claimed peptides of the invention, this

CC peptide exhibited no cell adhesion. The invention relates

CC to novel fibrinogen C-terminal peptides, peptide-09 (AAV52600),

CC peptide-70 (AAV52693) and peptide-71 (AAV52694). These claimed

CC peptides have cell adhesive effects, with peptide-09 being the most

CC potent for cell binding, and peptide-71 being the next most potent.

CC Peptide-71 was also found to have cell proliferative effects. The

CC peptides can be used to promote healing of a wound in a patient. They

CC can also be used for diseases characterised by the absence of a

CC cellular product, e.g., diabetes mellitus type I, haemophilia A

CC (factor VIII deficiency), and haemophilia B (factor IX deficiency).

CC They can also be used for the growth and transport of cells in cell

CC culturing systems, the separation of different types of cells from

CC mixed cell cultures, and the transplantation of cells into tissues

CC or cell cultures. They can be used for producing therapeutic structures,

CC e.g., gels, prosthetic devices or collagen sheets. The peptides can

CC also be used as tools for performing analysis of other physiological

CC systems, and for further research and development, for example, to

CC identify and isolate cell receptors. The peptides can also be used in

CC diagnosis, e.g., of blood coagulation disorders.

XX

SQ Sequence 19 AA;

Query Match 33.6%; Score 36; DB 21; Length 19;

Best Local Similarity 66.7%; Pred. No. 22;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 DHQGTSSK 11

Db 3 dhegthstk 11

RESULT 3

AAR67862

ID AAR67862 standard; peptide; 9 AA.

XX

AC AAR67862;

XX

DT 07-SEP-1995 (first entry)

XX

DE FVII/TF multi-protein complex inhibition test peptide FVII-4B.

XX

KW Factor VII; Factor 7; blood clotting factor; multi-protein complex;

KW human tissue factor; FVII/TF; assay.

XX

OS Synthetic.

XX

PN WO9500847-A.

XX

PD 05-JAN-1995.

XX

PF 17-JUN-1994; 94WO-GB01314.

XX

PR 18-JUN-1993; 93GB-0012638.

XX

PA (HAFS-) HAFSLUND NYCOMED AS.

PA (HOLM/) HOLMES M J.

XX

PI Oerning L, Sakariassen K, Stephens R;

XX

DR WPI; 1995-052226/07.

XX

PT Immunoassay for multi-protein complexes - used to detect

PT malfunction in formation of complexes in an individual, e.g. due

PT to genetic or physiological disorders

XX

PS Example 2; Page 8; 19pp; English.

XX

CC Synthetic peptides (AAR67858-R67865) were individually assayed as test

CC substances to ascertain their effect on the formation of the blood-

CC clotting factor VII/tissue factor multi-protein complex. Of the

CC peptides tested, the most inhibition was obtained with cyclic

CC peptides representing the ring structures present in the FVII growth

CC factor domains (i.e. AAR67861, AAR67864 and AAR67863). Peptide AAR67858,

CC a linear peptide corresp. to residues 136-146 from a region close to

CC the site of cleavage which activates FVII also had good inhibitory

CC activity.

XX

SQ Sequence 9 AA;

Query Match 29.9%; Score 32; DB 16; Length 9;
 Best Local Similarity 75.0%; Pred. No. 3.4e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 DHQGTSS 10
 |||||
 Db 2 dhtgltks 9

RESULT 4

AAR68909
 ID AAR68909 standard; peptide; 9 AA.

XX AAR68909;

XX 06-AUG-1995 (first entry)

XX Factor-VII-derived peptide fragment FVII-4B.

XX Factor-VII; blood-clotting factor; thrombosis; angina;
 XX cerebrovascular disease; pulmonary embolism; heart disease.

XX Synthetic.

XX W09500541-A.

XX 05-JAN-1995.

XX 17-JUN-1994; 94WO-GB01315.

XX 18-JUN-1993; 93GB-0012601.

XX 10-MAY-1994; 94GB-0009335.

XX (HAFS-) HAFSLUND NYCOMED AS.

XX (HOLM/) HOLMES M J.

XX Oerling L, Sakariassen KS, Stephens RW, Sakariassen K;

XX WPI; 1995-052003/07.

XX Factor VII-derived peptide compounds - useful for

XX preventing/inhibiting binding of tissue factor to factor VII.

XX Disclosure: Page 20; 61pp; English.

XX This peptide fragment is useful for preparing pharmaceutical

XX compositions for prevention or inhibition of Factor-VII binding to

XX tissue factor. It is useful for treating or preventing blood clotting

XX disorders in humans and animals, e.g. thrombosis, angina,

XX cerebrovascular disease or pulmonary embolism.

XX Sequence 9 AA;

OY 3 DHQGTSS 10
 |||||
 Db 2 dhtgltks 9

RESULT 5

AAR05852
 ID AAR05852 standard; protein; 11 AA.

XX AAR05852;

XX 06-SEP-1990 (first entry)

XX Factor VII peptide analogue.

KW Factor VII; blood clotting; Tissue factor; TF; thrombosis.

XX Synthetic.

XX W09003390-A.

XX 05-APR-1990.

XX 22-SEP-1989; 89WO-0004140.

XX 23-SEP-1988; 88US-0248817.

XX (CORV-) CORVAS INC.

XX Pepe MG;

XX WPI; 1990-132239/17.

XX New clotting factor VII peptide analogues -

XX useful for inhibiting blood clotting induced by tissue factor

XX complex.

XX Claim 11; Page 22; 28pp; English.

XX One or both of the two C-terminal residues may be absent, the

XX peptide is useful in inhibiting formation of active tissue factor:

XX factor VII complex and thus blood clotting.

XX Sequence 11 AA;

OY 3 DHQGTSS 10
 |||||
 Db 3 dhtgltks 10

Query Match 29.9%; Score 32; DB 11; Length 11;
 Best Local Similarity 75.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 6

AAR67860
 ID AAR67860 standard; peptide; 11 AA.

XX AAR67860;

XX 07-SEP-1995 (first entry)

XX FVII/TF multi-protein complex inhibition test peptide FVII-4.

XX Factor VII; Factor 7; blood clotting factor; multi-protein complex;

XX human tissue factor; FVII/TF; assay.

XX Synthetic.

XX W09500847-A.

XX 05-JAN-1995.

XX 17-JUN-1994; 94WO-GB01314.

XX 18-JUN-1993; 93GB-0012638.

XX (HAFS-) HAFSLUND NYCOMED AS.

XX (HOLM/) HOLMES M J.

XX Oerling L, Sakariassen K, Stephens R;

XX WPI; 1995-052226/07.

XX Immunoassay for multi-protein complexes - used to detect

XX malfunction in formation of complexes in an individual, e.g. due

XX to genetic or physiological disorders

XX Example 2; Page 8; 19pp; English.

XX Synthetic peptides (AAR67858-R67865) were individually assayed as test

CC substances to ascertain their effect on the formation of the blood-

CC clotting factor VII/tissue factor multi-protein complex. Of the

CC peptides tested, the most inhibition was obtained with cyclic

CC peptides representing the ring structures present in the FVII growth

CC factor domains (i.e. AAR67861, AAR67864 and AAR67863). Peptide AAR67858,

CC a linear peptide corresp. to residues 136-146 from a region close to

CC the site of cleavage which activates FVII also had good inhibitory

CC activity.

XX Sequence 11 AA;

SQ

Query Match 29.9%; Score 32; DB 16; Length 11;

Best Local Similarity 75.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DHOGTKSS 10

Db 2 dhtgtkrs 9

RESULT 7

AAR68908

ID AAR68908 standard; peptide; 11 AA.

XX AC AAR68908;

XX 06-AUG-1995 (first entry)

DT XX

DE XX

XX Factor-VII-derived peptide fragment FVII-4.

XX Factor-VII; blood-clotting factor; thrombosis; angina;

KW cerebrovascular disease; pulmonary embolism; heart disease.

XX Synthetic.

XX OS

XX WO9500541-A.

PN 05-JAN-1995.

PD XX

XX 17-JUN-1994; 94WO-GB01315.

PF XX

PR 18-JUN-1993; 93GB-0012601.

PR 10-MAY-1994; 94GB-0009335.

XX (HAFS-) HAFSLJND NYCOMED AS.

PA (HOLM/) HOLMES M J.

PA Orning L, Sakariassen KS, Stephens RW, Sakariassen K;

PI WPI; 1995-052003/07.

XX Factor VII-derived peptide compounds - useful for

PT preventing/inhibiting binding of tissue factor to factor VII.

XX Disclosure; Page 20; 61pp; English.

XX This peptide fragment is useful for preparing pharmaceutical

CC compositions for prevention or inhibition of Factor-VII binding to

CC tissue factor. It is useful for treating or preventing blood clotting

CC disorders in humans and animals, e.g. thrombosis, angina,

CC cerebrovascular disease or pulmonary embolism.

XX Sequence 11 AA;

SQ

Query Match 29.9%; Score 32; DB 16; Length 11;

Best Local Similarity 75.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DHOGTKSS 10

Db 2 dhtgtkrs 9

RESULT 8

AAW85479

ID AAW85479 standard; Peptide; 14 AA.

XX AC AAW85479;

XX 15-MAR-1999 (first entry)

DT XX

DE XX

XX Mouse GP88 autocrine growth factor antigenic peptide SI4R.

XX GP88; granulio; epithilin; mouse; growth factor; autocrine; tumour;

KW cancer; viral infection; antagonist; therapy; diagnosis; antigen;

KW antibody.

XX Mus sp.

XX OS

XX WO9852607-Al.

PN 26-NOV-1998.

PD XX

XX 22-MAY-1998; 98WO-US10555.

PF XX

PR 16-DEC-1997; 97US-0991862.

PR 23-MAY-1997; 97US-0863079.

XX (SERR/) SERRERO G.

PA Serrero G;

PI WPI; 1999-045276/04.

XX Composition containing antagonist of growth factor GP88 - useful for

PT treating cancer and viral diseases and also for diagnosing disease

PT from altered GP88 expression

XX Example 8; Page 45; 86pp; English.

XX This is the amino acid sequence of peptide SI4R, comprising amino

CC acid residues S562-R575 of murine GP88 (see AAW85474). GP88 is an 88

CC kDa glycoprotein autocrine growth factor that is expressed in a

CC tightly regulated manner in normal cells, is overexpressed and

CC unregulated in highly tumorigenic cells derived from normal cells,

CC and which acts as a stringently required growth stimulator for the

CC tumorigenic cells. SI4R was used to raise neutralising antibodies

CC to GP88. Antagonists to GP88, such as anti-GP88 antibodies, are

CC used to treat diseases associated with increased expression of

CC GP88, particularly cancer but also viral infections. Anti-GP88

CC antibodies can also be used as diagnostic reagents and to deliver

CC toxins or other compounds to GP88-expressing cells.

XX Sequence 14 AA;

SQ

Query Match 29.9%; Score 32; DB 20; Length 14;

Best Local Similarity 40.0%; Pred. No. 74;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 8 KSSKCVROKV 17

Db 3 rgtkcirkki 12

RESULT 9

AAW86759

ID AAY86759 standard; Peptide; 9 AA.

XX AC AAY86759;

XX 05-MAY-2000 (first entry)
XX
XX Telomerase peptide #174.
DE
XX Telomerase: antigenic peptide; cancer; therapy; human; tumour cell;
KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
KW telomerase T lymphocyte.
XX
OS Homo sapiens.
XX
XX WO200002581-A1.
XX
XX 20-JAN-2000.
XX
XX 30-JUN-1999; 99WO-N000220.
XX
XX 08-JUL-1998; 98NO-0003141.
XX
XX (NHVD) NORSK HYDRO AS.
XX
XX Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
PI Saebøe-Larsen S;
XX
XX WPI: 2000-145727/13.
XX
XX Protein or peptide fragments useful in the treatment and prophylaxis of
PT cancer in mammals -
XX
XX Claim 12; Page 35; 53pp: English.
XX
XX This sequence represents a telomerase peptide of the invention, and can
CC be used in a method for the treatment or prophylaxis of cancer. The
CC sequences are useful in the treatment or prophylaxis of cancer
CC especially, breast, lung, ovarian, cervical, colorectal, prostate or
CC pancreatic cancers, malignant melanoma, leukaemias, lymphomas, or biliary
CC tract carcinomas. They are useful for generating telomerase T lymphocytes
CC capable of recognising and destroying tumour cells in a mammal,
CC comprising culturing T lymphocytes obtained from the mammal with the
CC peptides. Telomerase protein is expressed only by tumour cells, hence,
CC other body cells are not targeted or destroyed by telomerase specific T
CC cells.
CC Note: This sequence was indexed from WO200002581, which is the first
CC major country equivalent to NO9803141.
XX
XX Sequence 9 AA:
SQ

Query Match 29.0%; Score 31; DB 21; Length 9;
Best Local Similarity 55.6%; Pred. NO. 3.4e+05;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 12 CVROKVEGS 20
I I I I I I
Db 1 carekpgs 9

RESULT 10
AAW55855
ID AAW55855 standard; peptide; 20 AA.
XX
XX AAW55855;
XX
XX 21-JUL-1998 (first entry)
XX
XX HIV p17 gag protein antigenic peptide HIV-1HAN.
XX
XX HIV; human immunodeficiency virus; antigen; conjugated peptide;
KW p17 gag protein; T cell specific binding peptide; TH1; TH2; AIDS;
KW Immune response; HGP-30.
XX
XX Human immunodeficiency virus type 1.
XX

PN WO9806416-A1.
XX
XX 19-FEB-1998.
PD
XX 08-AUG-1997; 97WO-US13901.
PF
XX 09-AUG-1996; 96US-0695304.
PR
XX (CELS-) CEL-SCI CORP.
XX
XX Sarin PS, Zimmerman DS;
XX
XX WPI: 1998-159280/14.
XX
XX New conjugated peptide(s) for treating or preventing HIV infection -
PT comprise first and second T cell specific peptide(s) with one
PT peptide having a sequence derived from HIVp17gag protein
XX
XX Disclosure; Page 10; 58pp: English.
XX
XX The present sequence represents an HIV p17 gag protein antigenic
CC peptide species specific sequence from the present invention. The
CC present invention describes a conjugated peptide which is capable
CC of eliciting a TH1 response when administered to a human. The
CC conjugated peptide comprises a first T cell specific binding peptide
CC (SBP), and a second T cell SBP, the first and second peptides being
CC derived from different molecules and covalently linked together, where
CC the first T cell SBP binds to a specific class or subclass of T cells
CC and the second T cell SBP is an antigenic peptide capable of eliciting
CC TH1 associated antibodies and having sequence identity with the p17 gag
CC protein of HIV where the peptide has a sequence originating with an
CC amino acid residue chosen from residues 75 to 82 and ending with an
CC amino acid residue chosen from residues 106 to 111 of p17 gag protein of
CC HIV. The peptides can induce a TH1, TH2 or mixed TH1/TH2 directed immune
CC response against HIV and HIV infected cells. They can be used for
CC treating or preventing HIV infection and AIDS.
XX
XX Sequence 20 AA:
SQ

Query Match 29.0%; Score 31; DB 19; Length 20;
Best Local Similarity 71.4%; Pred. NO. 1.6e+07;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 12 CVROKVE 18
I I I I I I
Db 12 cvnqkie 18

RESULT 11
AAW55845
ID AAW55845 standard; peptide; 20 AA.
XX
XX AAW55845;
XX
XX 21-JUL-1998 (first entry)
XX
XX HIV p17 gag protein antigenic peptide HIV-1TB132.
XX
XX HIV; human immunodeficiency virus; antigen; conjugated peptide;
KW p17 gag protein; T cell specific binding peptide; TH1; TH2; AIDS;
KW Immune response; HGP-30.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO9806416-A1.
XX
XX 19-FEB-1998.
PD
XX 08-AUG-1997; 97WO-US13901.
PF
XX 09-AUG-1996; 96US-0695304.
PR
XX

CC conjugated peptide comprises a first T cell specific binding peptide
CC (SBP), and a second T cell SBP, the first and second peptides being
CC derived from different molecules and covalently linked together, where
CC the first T cell SBP binds to a specific class or subclass of T cells
CC and the second T cell SBP is an antigenic peptide capable of eliciting
CC TH1 associated antibodies and having sequence identity with the p17 gag
CC protein of HIV where the peptide has a sequence originating with an
CC amino acid residue chosen from residues 75 to 82 and ending with an
CC amino acid residue chosen from residues 106 to 111 of p17 gag protein of
CC HIV. The peptides can induce a TH1, TH2 or mixed TH1/TH2 directed immune
CC response against HIV and HIV infected cells. They can be used for
CC treating or preventing HIV infection and AIDS.

XX Sequence 20 AA;

Query Match 29.0%; Score 31; DB 19; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVRQKVE 18
| | | | |
Db 12 cvnqkie 18

RESULT 14

AAB23773
ID AAB23773 standard; Peptide; 21 AA.

AC AAB23773;

DT 11-JAN-2001 (first entry)

DE Entry vector pENTR5 cloning site peptide sequence.

XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KM gene product targeting; fusion tag cleavage.

XX Bacteriophage lambda.
OS Synthetic.

XX WO200052027-A1.

XX 08-SEP-2000.

PF 02-MAR-2000; 2000MO-US05432.

XX 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

PA (LIFE-) LIFE TECHNOLOGIES INC.

XX Hartley JL, Brasch MA, Temple GF, Cheo D;

PI WPI; 2000-543948/49.

PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
recombinational cloning of polypeptides -

XX Example 4; Fig 14; 459pp; English.

XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of

CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

XX Sequence 21 AA;

Query Match 28.0%; Score 30; DB 21; Length 21;
Best Local Similarity 35.7%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 HOGTKSKRCVROKV 17
| | | | | : : :
Db 8 hmgtnsvdwiryr 21

RESULT 15

AAR35477
ID AAR35477 standard; peptide; 13 AA.

AC AAR35477;

DT 25-AUG-1993 (first entry)

DE Phosphatidylserine recognising peptide.

XX Inhibition; activity; blood coagulation factor VIII; thrombosis;
KW treatment; artificial membrane; medicinal artificial material.

XX Synthetic.

XX JP05092993-A.

XX 16-APR-1993.

PF 30-SEP-1991; 91JP-0276138.

PR 30-SEP-1991; 91JP-0276138.

XX (TOYJ) TOSOH CORP.

XX WPI; 1993-162126/20.

XX New physiologically active peptide recognising phosphatidylserine
PT and-ethanolamine - inhibits activity of blood coagulation factor VIII
PT but not factor V, used for treating thrombosis, etc.

XX Claim 2; Page 2; 6pp; Japanese.

XX The sequence is that of a peptide recognising phosphatidylserine
CC and -ethanolamine. It inhibits the activity of blood coagulation
CC factor VIII, and does not inhibit the activity of factor V. It is
CC useful in the treatment of blood coagulation disorders, e.g.
CC thrombosis, etc. It is also useful in the study of phosphatidylserine
CC which plays an important role in the cell membrane, artificial
CC membranes and medicinal artificial material.

XX Sequence 13 AA;

Query Match 27.1%; Score 29; DB 14; Length 13;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 14 RQVVEGS 20
|| ||||
Db 2 rqnvegs 8

Search completed: July 19, 2001, 07:47:34
Job time: 45 sec

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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:46:49 ; Search time 12.2 Seconds
(without alignments)
34.675 Million cell updates/sec

Title: US-08-487-283A-1

Perfect score: 107

Sequence: 1 VIDHGTKSKCYRQKVEGSS 21

Scoring table:
BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 105797

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCURS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	29.9	9	2	US-08-564-063-25
2	32	29.9	10	2	US-08-564-063-3
3	32	29.9	11	2	US-08-564-063-2
4	31	29.0	20	3	US-08-695-301A-18
5	31	29.0	20	3	US-08-695-301A-21
6	31	29.0	20	3	US-08-695-301A-24
7	31	29.0	20	3	US-08-695-301A-28
8	31	29.0	20	3	US-08-695-304C-18
9	31	29.0	20	3	US-08-695-304C-21
10	31	29.0	20	3	US-08-695-304C-24
11	31	29.0	20	3	US-08-695-304C-28
12	30	28.0	13	3	US-08-545-860D-70
13	30	28.0	13	5	PCR-US94-04486-70
14	29	27.1	14	1	US-08-769-309A-6
15	29	27.1	14	3	US-08-994-570-6
16	28	26.2	17	2	US-08-248-839C-66
17	28	26.2	20	3	US-08-695-301A-16
18	28	26.2	20	3	US-08-695-301A-19
19	28	26.2	20	3	US-08-695-301A-20
20	28	26.2	20	3	US-08-695-301A-22
21	28	26.2	20	3	US-08-695-301A-23
22	28	26.2	20	3	US-08-695-301A-26
23	28	26.2	20	3	US-08-695-301A-27
24	28	26.2	20	3	US-08-695-301A-29
25	28	26.2	20	3	US-08-695-301A-31
26	28	26.2	20	3	US-08-695-301A-32
27	28	26.2	20	3	US-08-695-301A-33

28	28	26.2	20	3	US-08-695-301A-34	Sequence 34, Appl
29	28	26.2	20	3	US-08-695-304C-16	Sequence 16, Appl
30	28	26.2	20	3	US-08-695-304C-19	Sequence 19, Appl
31	28	26.2	20	3	US-08-695-304C-20	Sequence 20, Appl
32	28	26.2	20	3	US-08-695-304C-22	Sequence 22, Appl
33	28	26.2	20	3	US-08-695-304C-23	Sequence 23, Appl
34	28	26.2	20	3	US-08-695-304C-27	Sequence 27, Appl
35	28	26.2	20	3	US-08-695-304C-29	Sequence 29, Appl
36	28	26.2	20	3	US-08-695-304C-31	Sequence 31, Appl
37	28	26.2	20	3	US-08-695-304C-32	Sequence 32, Appl
38	28	26.2	20	3	US-08-695-304C-33	Sequence 33, Appl
39	28	26.2	20	3	US-08-695-304C-34	Sequence 34, Appl
40	27	25.2	14	2	US-08-908-526-5	Sequence 5, Appl
41	27	25.2	15	2	US-08-429-964-75	Sequence 75, Appl
42	27	25.2	19	2	US-08-637-759B-290	Sequence 290, App
43	27	25.2	19	3	US-08-871-355A-290	Sequence 290, App
44	27	25.2	20	4	US-08-840-006-4	Sequence 4, Appl
45	27	25.2	21	4	US-09-179-558-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-564-063-25
; Sequence 25, Application US/08564063
; Patent No. 5962418
; GENERAL INFORMATION:
; APPLICANT: SAKARIASSEN, Kjell S
; APPLICANT: STEPHENS, Ross W
; APPLICANT: ORNING, Lars
; TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Testa, Hurwitz & Thibault, LLP
; STREET: 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,063
; FILING DATE: 28-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, Paula A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FRD-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-564-063-25

Query Match 29.9%; Score 32; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;
Gy 3 DHGCTKSS 10
Db 2 DHTGTRKS 9

```

RESULT      2
US-08-564-063-3
; Sequence 3, Application US/08564063
; Patent No. 5962418
; GENERAL INFORMATION:
; APPLICANT: SAKARIASSEN, Kjell S
; APPLICANT: STEPHENS, Ross W
; APPLICANT: ORNING, Lars
; TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault, LLP
; STREET: 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,063
; FILING DATE: 28-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, Paula A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FRD-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-564-063-3

Query Match      29.9%; Score 32; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 DHQGTKSS 10
        || ||| |
Db      2 DHTGTRKS 9

RESULT      3
US-08-564-063-2
; Sequence 2, Application US/08564063
; Patent No. 5962418
; GENERAL INFORMATION:
; APPLICANT: SAKARIASSEN, Kjell S
; APPLICANT: STEPHENS, Ross W
; APPLICANT: ORNING, Lars
; TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault, LLP
; STREET: 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1TBI32
US-08-695-301A-18

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVROKVE 18
|||11:1
Db 12 CVHOKIE 18

RESULT 5
US-08-695-301A-21
Sequence 21, Application US/08695301A
Patent No. 6093400

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,301A
FILING DATE: August 9, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
FEATURE:

NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1MN
US-08-695-301A-21

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVROKVE 18
|||11:1
Db 12 CVHOKIE 18

RESULT 6

US-08-695-301A-24
Sequence 24, Application US/08695301A
Patent No. 6093400

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,301A
FILING DATE: August 9, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
FEATURE:

NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1DY1
US-08-695-301A-24

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVROKVE 18
|||11:1
Db 12 CVHOKIE 18

RESULT 7
US-08-695-301A-28
Sequence 28, Application US/08695301A
Patent No. 6093400

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage

;; MEDIUM TYPE: 3.5 inch, 1.44 mb storage
;; COMPUTER: Dell System 210; Intel 80 286 Microprocessor
;; OPERATING SYSTEM: MS DOS 6.22
;; SOFTWARE: Word Perfect, Version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/695,301A
;; FILING DATE: August 9, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard A. Steinberg
;; REGISTRATION NUMBER: 26,588
;; REFERENCE/DOCKET NUMBER: CELL-101
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 549-2282
;; TELEFAX: (703) 836-0106
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 75 to 94
;; OTHER INFORMATION: fragment of p-17 gag protein of
;; HIV-1HAN
US-08-695-301A-28

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVRQKVE 18
|| ||:|
Db 12 CVHQKIE 18

RESULT 8
US-08-695-304C-18
;; Sequence 18, Application US/08695304C
;; Patent No. 6103239
;; GENERAL INFORMATION:
;; APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
;; TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
;; TITLE OF INVENTION: Compositions and Methods of Use
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Law Office of Sherman and Shalloway
;; STREET: 413 N. Washington Street
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
;; MEDIUM TYPE: 3.5 inch, 1.44 mb storage
;; COMPUTER: Dell System 210; Intel 80 286 Microprocessor
;; OPERATING SYSTEM: MS DOS 6.22
;; SOFTWARE: Word Perfect, Version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/695,304C
;; FILING DATE: August 9, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard A. Steinberg
;; REGISTRATION NUMBER: 26,588
;; REFERENCE/DOCKET NUMBER: CELL-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 549-2282
;; TELEFAX: (703) 836-0106
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 75 to 94
;; OTHER INFORMATION: fragment of p-17 gag protein of
;; HIV-ITB132
US-08-695-304C-18

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVRQKVE 18
|| ||:|
Db 12 CVHQKIE 18

RESULT 9
US-08-695-304C-21
;; Sequence 21, Application US/08695304C
;; Patent No. 6103239
;; GENERAL INFORMATION:
;; APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
;; TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
;; TITLE OF INVENTION: Compositions and Methods of Use
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Law Office of Sherman and Shalloway
;; STREET: 413 N. Washington Street
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
;; MEDIUM TYPE: 3.5 inch, 1.44 mb storage
;; COMPUTER: Dell System 210; Intel 80 286 Microprocessor
;; OPERATING SYSTEM: MS DOS 6.22
;; SOFTWARE: Word Perfect, Version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/695,304C
;; FILING DATE: August 9, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard A. Steinberg
;; REGISTRATION NUMBER: 26,588
;; REFERENCE/DOCKET NUMBER: CELL-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 549-2282
;; TELEFAX: (703) 836-0106
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 75 to 94
;; OTHER INFORMATION: fragment of p-17 gag protein of
;; HIV-1MN
US-08-695-304C-21

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVRQKVE 18

Db 12 CVHOKIE 18

RESULT 10

US-08-695-304C-24
Sequence 24, Application US/08695304C
Patent No. 6103239

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN

TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
TITLE OF INVENTION: Compositions and Methods of Use

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway

STREET: 413 N. Washington Street
CITY: Alexandria

STATE: Virginia
COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage

MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor

OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,304C

FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:

NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588

TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: CELL-102

TELEPHONE: (703) 836-0106
FAX: (703) 836-0106

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide

FRAGMENT TYPE: Internal fragment
FEATURE:

NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of

OTHER INFORMATION: HIV-1DVI
US-08-695-304C-24

Query Match 29.0%; Score 31; DB 3; Length 20;

Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVHOKIE 18
Db 12 CVHOKIE 18

RESULT 11

US-08-695-304C-28
Sequence 28, Application US/08695304C
Patent No. 6103239

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN

TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
TITLE OF INVENTION: Compositions and Methods of Use

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway

STREET: 413 N. Washington Street
CITY: Alexandria

STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage

MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor

OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,304C

FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:

NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588

REFERENCE/DOCKET NUMBER: CELL-102
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-0106
FAX: (703) 836-0106

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide

FRAGMENT TYPE: Internal fragment
FEATURE:

NAME/KEY:
LOCATION: 75 to 94

OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1HAN
US-08-695-304C-28

Query Match 29.0%; Score 31; DB 3; Length 20;

Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVHOKIE 18
Db 12 CVHOKIE 18

RESULT 12

US-08-545-860D-70
Sequence 70, Application US/08545860D
Patent No. 6040140

GENERAL INFORMATION:
APPLICANT: Croce, Carlo

TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewitz &

STREET: One Liberty Place, 46th floor
CITY: Philadelphia

STATE: Pennsylvania
COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/04496

;; FILING DATE: 22-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/10930
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/327,392
;; FILING DATE: 19-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/320,559
;; FILING DATE: 11-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/062,443
;; FILING DATE: 14-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/971,094
;; FILING DATE: 30-OCT-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/888,839
;; FILING DATE: 27-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/805,093
;; FILING DATE: 11-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeLuca Esq., Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1262
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 70:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-545-860D-70

Query Match 28.0%; Score 30; DB 3; Length 13;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 SKCVRQKVEGS 20
:||||| |
Db 3 TKCVRCCKSGS 13

RESULT 13
PCT-US94-04496-70
;; Sequence 70, Application PC/TUS9404496
;; GENERAL INFORMATION:
;; APPLICANT: Croce, Carlo
;; APPLICANT: Canaani, Eli
;; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
;; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
;; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
;; NUMBER OF SEQUENCES: 86
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
;; ADDRESSEE: Norris
;; STREET: One Liberty Place, 46th floor
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/04496
;; FILING DATE:

;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeLuca Esq., Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1242
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 70:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US94-04496-70

Query Match 28.0%; Score 30; DB 5; Length 13;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 SKCVRQKVEGS 20
:||||| |
Db 3 TKCVRCCKSGS 13

RESULT 14
US-08-769-309A-6
;; Sequence 6, Application US/08769309A
;; Patent No. 5741890
;; GENERAL INFORMATION:
;; APPLICANT: Scott, John D.,
;; APPLICANT: Nauert, Brian J.,
;; APPLICANT: Klauack, Theresa M.
;; TITLE OF INVENTION: Protein Binding Domains of Gravin
;; NUMBER OF SEQUENCES: 24
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower/233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/769,309A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5741890and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/33451
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-474-6300
;; TELEFAX: 312-474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-769-309A-6

Query Match 27.1%; Score 29; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 7 TKSSKCVRKVE 18
 ||||| |:::
 Db 3 TKSSKLVQNIQ 14

RESULT 15

US-08-994-570-6
 ; Sequence 6, Application US/08994570
 ; Patent No. 6090929
 ; GENERAL INFORMATION:
 ; APPLICANT: Scott, John D.,
 ; APPLICANT: Nauert, Brian J.,
 ; APPLICANT: Klauck, Theresa M.
 ; TITLE OF INVENTION: Protein Binding Domains of Gravin
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower/233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/994,570
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6090929and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/33451
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-994-570-6

Query Match 27.1%; Score 29; DB 3; Length 14;
 Best Local Similarity 50.0%; Pred. No. 98;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 7 TKSSKCVRKVE 18
 ||||| |:::
 Db 3 TKSSKLVQNIQ 14

Search completed: July 19, 2001, 07:47:09
 Job time: 20 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:49:39 ; Search time 12.68 Seconds

(without alignments)
30.037 Million cell updates/sec

Title: US-08-487-283A-1_COPY_8_12

Perfect score: 27

Sequence: 1 KSKC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	37.0	4	2	PT0534
2	10	37.0	4	2	S55238
3	10	37.0	5	2	A33882
4	10	37.0	5	2	B45525
5	10	37.0	5	2	S65726
6	10	37.0	5	2	PT0577
7	10	37.0	5	2	PT0565
8	10	37.0	5	2	PT0700
9	9	33.3	3	2	A22565
10	9	33.3	4	2	I40505
11	9	33.3	4	2	I51049
12	9	33.3	4	2	S43959
13	9	33.3	5	2	D60274
14	9	33.3	5	2	B22565
15	9	33.3	5	2	F22565
16	9	33.3	5	2	S11127
17	9	33.3	5	2	PT0295
18	9	33.3	5	2	PT0308
19	9	33.3	5	2	PT0610
20	9	33.3	5	2	PT0660
21	9	33.3	5	2	PT0535
22	9	33.3	5	2	PT0684
23	8	29.6	3	2	PT0622
24	8	29.6	4	2	PT0696
25	8	29.6	4	2	PT0645
26	8	29.6	4	2	PT0712
27	8	29.6	4	2	PT0698
28	8	29.6	4	2	PT0551
29	8	29.6	4	2	A40135

30	8	29.6	5	2	I40698	biotin B - Citroba
31	8	29.6	5	2	A37114	hypoxanthine phosph
32	8	29.6	5	2	PT0596	T-cell receptor be
33	8	29.6	5	2	PT0597	T-cell receptor be
34	8	29.6	5	2	PT0644	T-cell receptor be
35	8	29.6	5	2	PT0600	T-cell receptor be
36	8	29.6	5	2	PT0729	T-cell receptor be
37	8	29.6	5	2	PT0624	T-cell receptor be
38	8	29.6	5	2	PT0686	T-cell receptor be
39	8	29.6	5	2	PT0601	T-cell receptor be
40	8	29.6	5	2	PT0625	T-cell receptor be
41	8	29.6	5	2	PT0672	T-cell receptor be
42	8	29.6	5	2	PT0656	T-cell receptor be
43	8	29.6	5	2	PT0659	T-cell receptor be
44	8	29.6	5	2	PT0699	T-cell receptor be
45	8	29.6	5	2	PT0561	T-cell receptor be

ALIGNMENTS

RESULT 1
PT0534
T-cell receptor beta chain V-D-J region (126-1AC) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0534
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0534
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <REP>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 37.0%: Score 10; DB 2; Length 4;
Best Local Similarity 66.7%: Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSK 4
DB 1 ASK 3

RESULT 2
S55238
pallidipin - assassin bug (fragment)
C:Species: Triatoma pallidipennis (assassin bug)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: S55238
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schlen
Biochem. J. 307, 465-470, 1995
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation in
A:Reference number: S55238; MUID:95251610
A:Accession: S55238
A:Molecule type: protein
A:Residues: 1-4 <HAE>

Query Match 37.0%: Score 10; DB 2; Length 4;
Best Local Similarity 50.0%: Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KC 5
DB 2 EC 3

RESULT 3

A33882
 cadmium-binding pentapeptide - downy thornapple
 C:Species: Datura innoxia (downy thornapple)
 C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
 C:Accession: A33882
 R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
 A:Title: Poly(gamma-glutamylcysteinylglycine: its role in cadmium resistance in plant
 A:Reference number: A94182; MUID:88016144
 A:Accession: A33882
 A:Molecule type: protein
 A:Residues: 1-5 <JAC>

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KC 5
 :|
 Db 1 EC 2

RESULT 4
 B45525
 actin I - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
 C:Accession: B45525
 R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmak
 Mol. Biochem. Parasitol. 35, 167-176, 1989
 A:Title: Stage-specific expression and genomic organization of the actin genes of the ma
 A:Reference number: A45525; MUID:89364996
 A:Accession: B45525
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <WES>
 A:Cross-references: GB:J03988
 A:Note: The authors translated the codon GAA for residue 3 as Gly
 C:Comment: The actin I gene contains no introns.

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KC 5
 :|
 Db 3 EC 4

RESULT 5
 S65726
 hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)
 C:Species: Lumbricus terrestris (common earthworm)
 C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C:Accession: S65726
 R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
 Biochim. Biophys. Acta 1292, 273-280, 1996
 A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobi
 A:Reference number: S65721; MUID:96176855
 A:Accession: S65726
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <FUS>

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KC 5
 :|
 Db 3 EC 4

Db 3 QC 4
 RESULT 6
 PT0577
 T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0577; PT0574
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A:Reference number: PT0509; MUID:91277601
 A:Accession: PT0577
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC
 A:Accession: PT0574
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FE2>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q
 C:Keywords: T-cell receptor

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSK 4
 :|
 Db 2 SSR 4

RESULT 7
 PT0565
 T-cell receptor beta chain V-D-J region (141-1CF) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0565
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A:Reference number: PT0509; MUID:91277601
 A:Accession: PT0565
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSK 4
 :|
 Db 2 SSR 4

RESULT 8
 PT0700
 T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0700
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A:Reference number: PT0509; MUID:91277601
 A:Accession: PT0700

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 37.0%; Score 10; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSK 4
DB 2 SSR 4

RESULT 9
A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 33.3%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 C 5
DB 1 C 1

RESULT 10
I40505
Hypothetical protein 3 (4 aa) - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40505
R:Waye, M.M.; Winter, G.
Eur. J. Biochem. 158, 505-510, 1986
A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase gene of Bacillus stearothermophilus.
A:Reference number: I40503; MUID:86274732
A:Accession: I40505
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1; PID:g580944

Query Match 33.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SK 4
DB 3 SK 4

RESULT 11
I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) metallothionein-A.
A:Reference number: I51049; MUID:95324545
A:Accession: I51049
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 33.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 C 5
DB 4 C 4

RESULT 12
S43959
Ig mu chain V region (clone 13) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036
A:Accession: S43959
A:Molecule type: DNA
A:Residues: 1-4 <WAG>
C:Keywords: immunoglobulin

Query Match 33.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 C 5
DB 2 C 2

RESULT 13
D60274
major protein antigen MPN46 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: D60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the cult filtrate of Mycobacterium tuberculosis.
A:Reference number: A60274; MUID:91099989
A:Accession: D60274
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 33.3%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 SSK 4
DB 3 SK 5

RESULT 14
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri

C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601
A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match 33.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 C 5
|
Db 2 C 2

RESULT 15
F22565
R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: F22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601
A;Accession: F22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match 33.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 C 5
|
Db 3 C 3

Search completed: July 19, 2001, 07:51:23
Job time: 104 sec

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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:51:09 ; Search time 9.96 Seconds
(without alignments)
17.197 Million cell updates/sec

Title: US-08-487-283a-1_COPY_8_12

Perfect score: 27
Sequence: 1 KSKRC 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	29.6	5	1	BIOB_CITFR
2	7	25.9	5	1	TRM3_ECOLI
3	6	22.2	4	1	DCMS_PSECH
4	6	22.2	4	1	TOFT_HUMAN
5	5	18.5	3	1	GRWA_HUMAN
6	5	18.5	3	1	LUXE_VIBFI
7	5	18.5	4	1	EOSI_HUMAN
8	5	18.5	5	1	BPP7_BOTIN
9	4	14.8	4	1	RM01_YEAST
10	4	14.8	5	1	AL14_CARMA
11	4	14.8	5	1	UXA4_CHLTR
12	3	11.1	5	1	BIOB_SALTY
13	3	7.4	4	1	PAR3_HIRME
14	2	7.4	4	1	PAR4_HIRME
15	2	7.4	4	1	FLRF_HIRME
16	2	7.4	4	1	FMRE_MACNI
17	2	7.4	5	1	BIOA_CITFR
18	2	7.4	5	1	BIOA_SALTY
19	2	7.4	5	1	PARP_ARTTR
20	2	7.4	5	1	PRCT_PPRAM
21	2	7.4	5	1	SUGA_ACHDO
22	2	7.4	5	1	TPIS_CANFA
23	2	7.4	5	1	UP01_MOUSE
24	1	3.7	3	1	THYL_PIG
25	1	3.7	4	1	ACH1_ACHFU
26	0	0.0	4	1	DCML_PSECH
27	0	0.0	4	1	PAP2_PARMA
28	0	0.0	5	1	PAR2_PARMA

ALIGNMENTS

RESULT 1
BIOB_CITFR
ID BIOB_CITFR STANDARD: PRT: 5 AA.
AC P12997;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).
GN BIOB.
OS Citrobacter freundli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter
OX NCBI_TaxID=546;
RN [1]
RP MEDLINE=89006280; PubMed=2971595;
RA Shivan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundli and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) - BIOTIN.
CC -1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
FAMILY.
CC
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CC
CC EMBL: M21922; NOT ANNOTATED.CDS.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT NON_TER
SQ SEQUENCE 5 AA: 532 MW: 75A5B1ED6F0000 CRC64;

Query Match 29.6%; Score 8; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SS 3
DB 4 SS 5

RESULT 2
TRM3_ECOLI
ID TRM3_ECOLI STANDARD: PRT: 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE TRAM PROTEIN (FRAGMENT).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioaka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ
and traX genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONUGATION
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.

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 CC -----
 DR EMBL: M20941; ; NOT_ANNOTATED_CDS.
 DR PIR: A32014; A32014.
 KW Conjugation; Plasmid; DNA-binding.
 FT NON_TER 1
 SQ SEQUENCE 5 AA; 634 MW; 681B1AA443500000 CRC64;

Query Match 25.98; Score 7; DB 1; Length 5;
 Best Local Similarity 25.08; Pred. No. 9.3e+04;
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSK 4
 Db 1 KNDE 4

RESULT 3

DCMS_PSECH STANDARD; PRT; 4 AA.
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE CARBON MONOXIDE DEHYDROGENASE SMALL CHAIN (EC 1.2.99.2) (FRAGMENT).
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydophilic bacteria."
 RL Arch. Microbiol. 152:335-341(1989).
 CC -I- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
 CC ACCEPTOR.
 CC -I- COFACTOR: MOLYBDENUM.
 CC -I- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: PLO146; PLO146.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 420 MW; 60D33DD6F0000000 CRC64;

Query Match 22.28; Score 6; DB 1; Length 4;
 Best Local Similarity 50.08; Pred. No. 9.3e+04;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SK 4
 Db 2 AK 3

RESULT 4

ID TUFT_HUMAN STANDARD; PRT; 4 AA.
 AC P01858;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PHAGOCYTOSIS-STIMULATING PEPTIDE (TUFTSIN).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72187087; PubMed=4112769;
 RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
 RT "The characteristics, isolation and synthesis of the phagocytosis
 RT stimulating peptide tuftsin."
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
 RN [2]
 RP IMMUNOGLOBULIN CLASS.
 RX MEDLINE=68091045; PubMed=4169272;
 RA Fidalgo B.V., Najjar V.A.;
 RT "The physiological role of the lymphoid system. VI. The stimulatory
 RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
 RT activity of human polymorphonuclear leucocyte."
 RL Biochemistry 6:3386-3392(1967).
 CC -I- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
 CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
 CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
 CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
 CC ACTIVITY OF NEUTROPHILS.
 DR PIR: A02147; A02147.
 DR MIM; 191150; -.
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 22.28; Score 6; DB 1; Length 4;
 Best Local Similarity 50.08; Pred. No. 9.3e+04;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SK 4
 Db 1 TK 2

RESULT 5

ID GRWM_HUMAN STANDARD; PRT; 3 AA.
 AC P01157;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE GROWTH-MODULATING PEPTIDE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77162369; PubMed=858356;
 RA Schlesinger D.H., Pickart L., Thaler M.M.;
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine."
 RL Experientia 33:324-325(1977).
 CC -I- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
 CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
 DR PIR: A01421; GKHU
 SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 18.58; Score 5; DB 1; Length 3;
 Best Local Similarity 100.08; Pred. No. 9.3e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1
 Db 3 K 3

RESULT 6

ID LUXE_VIBFI STANDARD; PRT; 3 AA.
 AC P24272;


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DR 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE LONG-CHAIN-FATTY-ACID-LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19)
DE (ACYL-PROTEIN SYNTHETASE) (FRAGMENT).
GN LUXE.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon."
RL J. Bacteriol. 172:6797-6802(1990).
CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC -1- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN -> AMP + PYROPHOSPHATE
CC + AN ACYL-PROTEIN THIOLESTER.
CC -1- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
CC COMPLEX.
CC -----
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CC -----
DR EMBL: M62812; ? NOT ANNOTATED_CDS.
KW Luminescence; Ligase.
FT NON_TER 1
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 18.5%; Score 5; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1
Db 2 K 2

RESULT 7
BOSI_HUMAN STANDARD; PRT; 4 AA.
ID BOSI_HUMAN
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE EOSINOPHILOTOXIC PEPTIDES.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=106093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilotoxic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.

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DR PIR: A03190; ETHUL. 1 V -> A (IN OTHER PEPTIDE).
FT VARIANT 1
SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 18.5%; Score 5; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SR 4
Db 3 SE 4

RESULT 8
BPP7_BOTIN STANDARD; PRT; 5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR)
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=9035157; PubMed=2386615;
RX Citra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 18.5%; Score 5; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1
Db 2 K 2

RESULT 9
RM01_YEAST STANDARD; PRT; 4 AA.
ID RM01_YEAST
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L1 (YML1) (FRAGMENT).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reislin S.,

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RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RL subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR PIR: S17255; S17255.
DR SGD: L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 14.8%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2
DB 1 S 1

RESULT 10
AL14_CARMA STANDARD; PRT; 5 AA.
ID AL14_CARMA
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSSTATIN 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- SIMILARITY: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 14.8%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2
DB 2 S 2

RESULT 11
UXA4_CHLTR STANDARD; PRT; 5 AA.
ID UXA4_CHLTR
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/BU;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,

Query Match 11.1%; Score 3; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SK 4
DB 2 AR 3

RESULT 13
FAR3_HIRME STANDARD; PRT; 4 AA.
ID FAR3_HIRME
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
FT NON_TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

Query Match 14.8%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2
DB 2 S 2

RESULT 12
BIOB_SALTY STANDARD; PRT; 5 AA.
ID BIOB_SALTY
AC P12678;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).
GN BIOB.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shiuan D., Campbell A.;
RT "transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC -!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
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CC -----
DR EMBL: M21923; -; NOT_ANNOTATED_CDS.
DR StyGene; SGI0027; bioB.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT NON_TER 5
SQ SEQUENCE 5 AA; 611 MW; 7761F40DD6F00000 CRC64;

Query Match 11.1%; Score 3; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SK 4
DB 2 AR 3

RESULT 13
FAR3_HIRME STANDARD; PRT; 4 AA.
ID FAR3_HIRME
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

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DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OX Atychobdellida; Hirudiniformes; Hirudindae; Hirudo.
RN NCB1_TaxID=6421;
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Karlson M.A., Calabrese R.L.;
RT "Identification of Rfamid neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
KW FAMILY.
FT MOD_RES 4 AA; 598 MW; 69D4073B30000000 CRC64;
SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 7.4%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 K 1
DB 3 R 3

RESULT 14
FAR4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OX Atychobdellida; Hirudiniformes; Hirudindae; Hirudo.
RN NCB1_TaxID=6421;
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Karlson M.A., Calabrese R.L.;
RT "Identification of Rfamid neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
KW FAMILY.
FT MOD_RES 4 AA; 616 MW; 69D4068B30000000 CRC64;
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 7.4%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 K 1
DB 3 R 3

RESULT 15
FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FLRFAMIDE.
OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OX Atychobdellida; Hirudiniformes; Hirudindae; Hirudo.

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OX NCB1_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RC SPECIES=H.medicalinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Karlson M.A., Calabrese R.L.;
RT "Identification of Rfamid neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma trivolvis.";
RL Peptides 15:31-36(1994).
CC -! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
KW FAMILY.
FT MOD_RES 4 AA; 582 MW; 69D40729A0000000 CRC64;
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 7.4%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 K 1
DB 3 R 3

```

Search completed: July 19, 2001, 07:53:50
 Job time: 161 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:50:49 ; Search time 20.81 Seconds
(without alignments)
31.789 Million cell updates/sec

Title: US-08-487-283A-1_COPY_8_12
Perfect score: 27
Sequence: 1 KSKC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	25.9	5	10	Q99007 hordeum vul
2	5	18.5	5	11	Q08433 rattus norv
3	1	3.7	5	13	P82070 ittoria rub
4	1	3.7	5	13	P82071 ittoria rub
5	1	3.7	5	13	P82072 ittoria rub
6	1	3.7	5	13	P82073 ittoria rub
7	1	3.7	5	13	P82100 ittoria rub
8	0	0.0	5	13	P82099 ittoria rub

ALIGNMENTS

RESULT 1
ID Q99007 PRELIMINARY; PRT: 5 AA.
AC Q99007;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
OC Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HIMALAYA; TISSUE-ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
DR EMBL: X54643; CAA38455.1; -;
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 25.9%; Score 7; DB 10; Length 5;
Best Local Similarity 33.3%; Pred. No. 4.2e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSK 4
Db 2 ANK 4

RESULT 2
ID Q08433 PRELIMINARY; PRT: 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMblrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOAL (EC 2.4.1.17) (UDPCT)
DB (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROsome.
DR EMBL: S38636; AAB19259.1; -;
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 18.5%; Score 5; DB 11; Length 4;

Best Local Similarity 100.0%; Pred. No. 4.2e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1

Db 4 K 4

RESULT 3

P82070 ID P82070 PRELIMINARY; PRT; 5 AA.
AC P82070;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RT Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match

Best Local Similarity 3.7%; Score 1; DB 13; Length 5;

Mismatches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2

Db 5 A 5

RESULT 4

P82071 ID P82071 PRELIMINARY; PRT; 5 AA.
AC P82071;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE RUBELLIDIN 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RT Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.

KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 3.7%; Score 1; DB 13; Length 5;

Best Local Similarity 0.0%; Pred. No. 4.2e+05;

Mismatches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1

Db 2 E 2

RESULT 5

P82072 ID P82072 PRELIMINARY; PRT; 5 AA.
AC P82072;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE RUBELLIDIN 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RT Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 3.7%; Score 1; DB 13; Length 5;

Best Local Similarity 0.0%; Pred. No. 4.2e+05;

Mismatches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1

Db 2 E 2

RESULT 6

P82073 ID P82073 PRELIMINARY; PRT; 5 AA.
AC P82073;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE RUBELLIDIN 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";

RL Aust. J. Chem. 52:0-0(1999).
CC -1- FUNCTION: CARBIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 3.7%; Score 1; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.2e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 S 2
Db 5 T 5

RESULT 7
P82100 PRELIMINARY; PRT; 5 AA.
AC P82100;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DE ELECTRIN 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID-104895;
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 3.7%; Score 1; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.2e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 S 2
Db 3 T 3

RESULT 8
P82099 PRELIMINARY; PRT; 5 AA.
AC P82099;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DE ELECTRIN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID-104895;
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella".
RL Aust. J. Chem. 52:0-0(1999).

KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 0.0%; Score 0; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.2e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 K 1
Db 1 F 1

Search completed: July 19, 2001, 07:53:34
Job time: 165 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:47:59 ; Search time 17.33 Seconds

(without alignments)
17,491 Million cell updates/sec

Title: US-08-487-283A-1_COPY_8_12

Perfect score: 27

Sequence: 1 KSKC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 18613

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_0601.*
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21: /SID8/gcgdata/geneseq/AA2000.DAT.*
22: /SID8/gcgdata/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	81.5	5	20	AAV14283
2	22	81.5	5	20	AAV14251
3	22	81.5	5	21	AA15838
4	22	81.5	5	21	AA15855
5	22	81.5	5	22	AA17548
6	18	66.7	5	21	AA17208
7	17	63.0	5	21	AAV83309
8	16	59.3	5	21	AAV63087
9	16	59.3	5	22	AA172577
10	16	59.3	5	22	AA172592
11	16	59.3	5	22	AA17555

12	15	55.6	4	21	AA12055
13	15	55.6	5	11	AAV07335
14	15	55.6	5	11	AAV07336
15	15	55.6	5	16	AA177331
16	15	55.6	5	19	AA177359
17	15	55.6	5	19	AA177231
18	15	55.6	5	19	AA165315
19	15	55.6	5	21	AA165614
20	15	55.6	5	21	AA164348
21	14	51.9	3	21	AA151896
22	14	51.9	4	14	AA136615
23	14	51.9	4	14	AA136658
24	14	51.9	4	16	AA185513
25	14	51.9	4	17	AA15187
26	14	51.9	4	19	AA120407
27	14	51.9	4	19	AA161298
28	14	51.9	4	19	AA161134
29	14	51.9	4	19	AA13267
30	14	51.9	4	19	AA13268
31	14	51.9	4	19	AA13269
32	14	51.9	4	19	AA13270
33	14	51.9	4	19	AA13271
34	14	51.9	4	19	AA13272
35	14	51.9	4	19	AA13273
36	14	51.9	4	19	AA13274
37	14	51.9	4	19	AA13275
38	14	51.9	4	19	AA13276
39	14	51.9	4	19	AA13277
40	14	51.9	4	19	AA13278
41	14	51.9	4	19	AA13279
42	14	51.9	4	19	AA13284
43	14	51.9	4	20	AA130280
44	14	51.9	4	20	AA188038
45	14	51.9	4	20	AA188040

ALIGNMENTS

RESULT 1	
AA14283	AA14283 standard; peptide: 5 AA.
AC	AA14283:
XX	
DT	29-JUL-1999 (first entry)
XX	
DE	Chemokine peptide, LFL peptide2(6-10)[MCP-1].
XX	
KW	Chemokine; Immune response; monocyte chemoattractant protein-1; MCP-1;
KW	chemokine-induced activity; inflammatory response; vascular induction;
KW	haematopoietic cell-associated activity; tumour; coronary artery disease;
KW	myocardial infarction; unstable angina pectoris; atherosclerosis; asthma;
KW	vasculitis; lentiviral infection; low bone mineral density; suppressor;
KW	parasitic infection; autoimmune disease; psoriasis; wound healing;
KW	organ transplant rejection; rheumatoid arthritis; allergy; therapy;
KW	arachidonic acid pathway.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	W09912968-A2.
XX	
PD	18-MAR-1999.
XX	
PR	11-SEP-1998; 98WO-US19052.
XX	
PR	11-SEP-1997; 97US-0927939.
XX	
PA	(NEOR-) NEORX CORP.
XX	
PI	Granger DJ, Kanaly ST, Tatalick LM;
XX	

G4 GTPase motif fr
Matrix metallopro
Matrix metallopro
Human apolipoprote
ML-10 C-terminal
apL immunoreactive
Peptide #7. Synth
Desmoglein cell ad
Cadherin-related n
Biosactin T7232 sy
Group I synthetic
Group III synthetic
Antimicrobial tetr
Chelating moiety f
Human microtubule
Peptide 13 used to
Peptide 13 used to
Peptide #44 having
Peptide #45 having
Peptide #46 having
Peptide #47 having
Peptide #48 having
Peptide #49 having
Peptide #50 having
Peptide #51 having
Peptide #52 having
Peptide #53 having
Peptide #54 having
Peptide #55 having
Peptide #56 having
Peptide #11 having
Integrin alpha-v-b
Peptide used in th

DR WPI; 1999-347124/29.
 XX New chemokine peptides and mimetics
 XX
 XX Disclosure; Fig 14; 208pp; English.
 XX
 CC This sequence represents a fragment of the chemokine MCP-1.
 CC The invention relates to chemokine peptides and mimetics, particularly
 CC derived from monocyte chemoattractant protein-1 (MCP-1). The chemokine
 CC peptides and variants and derivatives can inhibit or reduce or increase,
 CC or enhance chemokine-induced activity. They can be used for increasing or
 CC enhancing an inflammatory response, an immune response or haematopoietic
 CC cell-associated activity at a tumour site. They can also be used for
 CC preventing or inhibiting an indication associated with haematopoietic
 CC cell recruitment or histamine release from basophils or mast cells. They
 CC can also be used to modulate the chemokine-induced activity of
 CC haematopoietic cells at a preselected physiological site, to treat a
 CC vascular indication, e.g. coronary artery disease, myocardial infarction,
 CC unstable angina pectoris, atherosclerosis, or vasculitis, lentiviral
 CC infection or replication in a vertebrate animal (e.g. malaria), an autoimmune
 CC disease, to suppress tumour growth in a vertebrate animal, to prevent or
 CC treat psoriasis in a mammal, to enhance wound healing, to prevent or
 CC treat asthma, organ transplant rejection, rheumatoid arthritis or
 CC allergy. They can also be used to inhibit a product or intermediate in
 CC the arachidonic acid pathway and where leukotriene, thromboxane and/or
 CC prostaglandin are inhibited and to prevent or inhibit an indication
 CC associated with elevated TNF-alpha.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 81.5%; Score 22; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSKC 5
 Db | | | |
 2 sskc 5

RESULT 2
 AAY14251
 ID AAY14251 standard; peptide; 5 AA.
 AC
 XX AAY14251;
 XX
 DT 29-JUL-1999 (first entry)
 XX
 XX Chemokine peptide, Peptide2(1-5)[MCP-1].
 DE
 DE Chemokine; immune response; monocyte chemoattractant protein-1; MCP-1;
 KW chemokine-induced activity; inflammatory response; vascular indication;
 KW haematopoietic cell-associated activity; tumour; coronary artery disease;
 KW myocardial infarction; unstable angina pectoris; atherosclerosis; asthma;
 KW vasculitis; lentiviral infection; low bone mineral density; suppressor;
 KW parasitic infection; autoimmune disease; psoriasis; wound healing;
 KW organ transplant rejection; rheumatoid arthritis; allergy; therapy;
 KW arachidonic acid pathway.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO9912968-A2.
 XX
 XX 18-MAR-1999.
 XX
 XX 11-SEP-1998; 98WO-US19052.
 XX
 XX 11-SEP-1997; 97US-0927939.
 XX
 XX (NEOR-); NEORX CORP.
 PA
 XX

PI Grainger DJ, Kanaly ST, Tatalick LM;
 XX WPI; 1999-347124/29.
 XX
 XX New chemokine peptides and mimetics
 XX
 XX Disclosure; Page 10; 208pp; English.
 XX
 CC This sequence represents a fragment of the chemokine hMCP-1.
 CC The invention relates to chemokine peptides and mimetics, particularly
 CC derived from monocyte chemoattractant protein-1 (MCP-1). The chemokine
 CC peptides and variants and derivatives can inhibit or reduce or increase,
 CC or enhance chemokine-induced activity. They can be used for increasing or
 CC enhancing an inflammatory response, an immune response or haematopoietic
 CC cell-associated activity at a tumour site. They can also be used for
 CC preventing or inhibiting an indication associated with haematopoietic
 CC cell recruitment or histamine release from basophils or mast cells. They
 CC can also be used to modulate the chemokine-induced activity of
 CC haematopoietic cells at a preselected physiological site, to treat a
 CC vascular indication, e.g. coronary artery disease, myocardial infarction,
 CC unstable angina pectoris, atherosclerosis, or vasculitis, lentiviral
 CC infection or replication in a vertebrate animal (e.g. malaria), an autoimmune
 CC disease, to suppress tumour growth in a vertebrate animal, to prevent or
 CC treat psoriasis in a mammal, to enhance wound healing, to prevent or
 CC treat asthma, organ transplant rejection, rheumatoid arthritis or
 CC allergy. They can also be used to inhibit a product or intermediate in
 CC the arachidonic acid pathway and where leukotriene, thromboxane and/or
 CC prostaglandin are inhibited and to prevent or inhibit an indication
 CC associated with elevated TNF-alpha.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 81.5%; Score 22; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSKC 5
 Db | | | |
 2 sskc 5

RESULT 3
 AAB15838
 ID AAB15838 standard; Peptide; 5 AA.
 XX
 XX AAB15838;
 XX
 XX 17-JAN-2001 (first entry)
 XX
 XX Human chemokine PF-4 SEQ ID NO: 90.
 DE
 DE Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;
 KW rheumatoid arthritis; contraception.
 XX
 XX Homo sapiens.
 OS
 XX WO200042071-A2.
 XX
 XX 20-JUL-2000.
 XX
 XX 12-JAN-2000; 2000WO-US00821.
 XX
 XX 12-JAN-1999; 99US-0229071.
 PR
 XX 17-MAR-1999; 99US-0271192.
 PR
 XX 01-DEC-1999; 99US-0452406.
 XX
 XX (NEOR-) NEORX CORP.
 PA
 XX

PI Granger DJ, Tatalick LM;
 XX WPI: 2000-499101/44.
 XX New peptide 3, amide and heterocyclic compounds and saccharide
 PT conjugates used for inhibiting chemokine induced activity and for
 PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
 PT growth
 XX
 XX Disclosure; Page 384; 387pp; English.
 PS
 XX The present invention concerns the identification of a number of
 CC chemokines which can be used to produce derivatives, agonists and
 CC antagonists which are then useful in disease treatment. The chemokines
 CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
 CC These chemokine derivatives can be used to treat diseases such as
 CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
 CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
 CC rheumatoid arthritis, and can be used to prevent strokes and as
 CC contraceptives. The coding sequences for the chemokines can be used in
 CC gene therapy for the same diseases, as well as in the production of
 CC animal models.
 CC
 XX Sequence 5 AA;

Query Match 81.5%; Score 22; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSKC 5
 ||||
 Db 2 sskc 5

RESULT 4
 AAB15855
 ID AAB15855 standard; peptide; 5 AA.
 XX
 AC AAB15855;
 XX
 DT 17-JAN-2001 (first entry)
 XX
 DE Human chemokine derived peptide #7.
 XX
 DE Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;
 KW rheumatoid arthritis; contraception.
 XX
 OS Synthetic.
 XX
 PN WO200042071-A2.
 XX
 PD 20-JUL-2000.
 XX
 PF 12-JAN-2000; 2000WO-US00821.
 XX
 PR 12-JAN-1999; 99US-0229071.
 PR 17-MAR-1999; 99US-0271192.
 PR 01-DEC-1999; 99US-0452406.
 XX
 PA (NEOR-) NEORX CORP.
 XX
 PI Granger DJ, Tatalick LM;
 XX WPI: 2000-499101/44.
 XX New peptide 3, amide and heterocyclic compounds and saccharide
 PT conjugates used for inhibiting chemokine induced activity and for
 PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour

PT growth
 XX
 PS Disclosure; Fig 18; 387pp; English.
 XX
 CC The present invention concerns the identification of a number of
 CC chemokines which can be used to produce derivatives, agonists and
 CC antagonists which are then useful in disease treatment. The chemokines
 CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
 CC These chemokine derivatives can be used to treat diseases such as
 CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
 CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
 CC rheumatoid arthritis, and can be used to prevent strokes and as
 CC contraceptives. The coding sequences for the chemokines can be used in
 CC gene therapy for the same diseases, as well as in the production of
 CC animal models.
 CC
 XX Sequence 5 AA;

OY 2 SSKC 5
 ||||
 Db 2 sskc 5

RESULT 5
 AAB37548
 ID AAB37548 standard; peptide; 5 AA.
 XX
 AC AAB37548;
 XX
 DT 01-MAR-2001 (first entry)
 XX
 DE CD8 activation complex SSK ridge analogue SC8-17.
 XX
 KW CD8 activation complex; cytotoxic T lymphocyte response; analogue;
 KW surface feature; gene therapy; diabetes; tissue transplantation.
 XX
 OS Unidentified.
 XX
 PN WO200066146-A1.
 XX
 PD 09-NOV-2000.
 XX
 PF 02-MAY-2000; 2000WO-US11902.
 XX
 PR 04-MAY-1999; 99US-0132361.
 PR 20-AUG-1999; 99US-0150150.
 PR 01-NOV-1999; 99US-0162632.
 XX
 PA (PHIL-) PHILADELPHIA HEALTH & EDUCATION CORP.
 XX
 PI Jameson BA, Tretiakova A;
 XX WPI: 2001-015912/02.
 XX
 PT Composition for inhibition of detrimental cytotoxic T lymphocyte
 PT responses comprising a compound that mimics or interacts with a surface
 PT feature of the CD8/MHC I complex
 XX
 PS Disclosure; Page 33; 40pp; English.
 XX
 CC The present invention provides compositions which can be used to inhibit
 CC detrimental cytotoxic T lymphocyte responses. These compounds mimic or
 CC interact with a surface feature (such as SHN, KIT, SSK, DEK and RPT) of
 CC the CD8/MHC I complex. This is useful in gene therapy, in the treatment of
 CC diabetes and in tissue transplantation.
 CC
 XX Sequence 5 AA;

Query Match 81.5%; Score 22; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSKC 5
 ||||
DB 2 sskc 5

RESULT 6
AAB17208
ID AAB17208 standard; Peptide; 5 AA.
XX
AC AAB17208;
XX
DT 31-OCT-2000 (first entry)
XX
DE IL-1 antagonist peptide sequence SEQ ID NO:264.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheatham J, Boone TC;
XX WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Claim 10; Page 289; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 5 AA;

Query Match 66.7%; Score 18; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSKK 4
 ||||
DB 2 kskk 5

RESULT 7
AAY83309
ID AAY83309 standard; Peptide; 5 AA.
XX
AC AAY83309;
XX
DT 16-AUG-2000 (first entry)
XX
DE Peptide motif of SDDL subtilisin-like serine protease.
XX
KW SDDL; serine protease; subtilisin; transgenic plants; dry weight;
KW stomata; sugar; water; protein; CO₂; H₂O; CO₂; H₂O;
KW crop protection; feed; foodstuffs.
XX
OS Synthetic.
OS Arabidopsis thaliana.
XX
PN WO200022144-A2.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-EP07633.
XX
PR 12-OCT-1998; 98EP-0119244.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
XX
PI Berger D, Altmann T;
XX WPI; 2000-317995/27.
XX
PT Novel recombinant DNA molecules encoding subtilisin-like serine
PT protease, useful for producing transgenic plants with altered stomata,
PT lower water consumption and enhanced diseased resistance
XX
PS Disclosure; Page 9; 101pp; English.
XX
CC Sequences encoding SDDL, a subtilisin-like serine protease, can be
CC used to produce transgenic plants with altered stomata
CC characteristics. These plants exhibit improved freshness,
CC increased dry weight, reduced leaf temperatures, reduced water loss
CC and lower water consumption and for enhancing the sugar and/or
CC protein content of plant leaves, modulating CO₂ uptake into and H₂O
CC release from leaves, for sustained photosynthesis under high
CC intensity conditions or for the improvement of disease resistance
CC of plants. The transgenic plants and cells of such plants are useful
CC in the preparation of feed, food or additives.
XX
SQ Sequence 5 AA;

Query Match 63.0%; Score 17; DB 21; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSKC 5
 ||||
DB 1 sssc 4

RESULT 8
AAY63087

ID AAY63087 standard; Peptide: 5 AA.
 AC AAY63087;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE LI-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:2629.
 XX
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW 08-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;
 KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PR-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 XX Disulfide-bond 1..5
 XX
 PN WO957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA00363.
 XX
 PR 05-MAY-1998; 98US-0073040.
 PR 06-NOV-1998; 980S-0187859.
 PR 20-JAN-1999; 99US-0234395.
 PR 08-MAR-1999; 99US-0264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-038791/03.
 XX
 PT New cadherin modulating agents, used for modulating nonclassical
 PT cadherin-mediated functions for treating e.g. cancers, obesity,
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
 PT disease
 XX
 PS Claim 78; Page 198; 252pp; English.
 XX
 CC The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue
 CC in a mammal. They can also be used for treating e.g. psoriasis,
 CC arthritis, age-related macular degeneration, multiple sclerosis and
 CC diabetes. The products can be used for detection and diagnosis and
 CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed
 CC peptides, and AAY64573 to AAY64643 and AA233183 to AA333186 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 5 AA;

Query Match 59.3%; Score 16; DB 21; Length 5;
 Best Local Similarity 50.0%; Pred. No. 3.4e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0;
 Gaps 0;
 Oy 2 SSKC 5
 Db 2 nkkc 5
 RESULT 9
 AAB72577
 ID AAB72577 standard; Peptide: 5 AA.
 XX
 AC AAB72577;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Thrombin-induced platelet activator antagonist #16.
 XX
 KW Platelet aggregation inhibitor; thrombin activation inhibitor;
 KW protease activated receptor 1; PAR1; platelet activation inhibitor;
 KW thrombosis; acute coronary syndrome.
 XX
 OS Unidentified.
 XX
 PN WO200112656-A1.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US40669.
 PF
 PR 17-AUG-1999; 99US-0375808.
 XX
 PA (THRO-) THROMGEN INC.
 XX
 PI Schmaier AH, Hasan AAK;
 XX
 DR WPI; 2001-226546/23.
 XX
 PT Inhibiting thrombin activation in human cell expressing protease
 PT activated receptor 1 (PAR1), comprises contacting mixtures of thrombin
 PT and human cell expressing PAR1, with a peptide that inhibits platelet
 PT activation
 XX
 PS Claim 7; Page 25; 49pp; English.
 XX
 CC The present invention relates to a method for inhibiting thrombin
 CC activation in a human cell expressing protease activated receptor 1
 CC (PAR1). The method involves using peptides (e.g. the present peptide)
 CC that inhibit platelet activation. The method is useful for preventing
 CC thrombosis and platelet aggregation. The method can be used for patients
 CC with acute coronary syndromes (e.g. crescendo angina, myocardial
 CC infarction) and for individuals who have acute coronary syndromes and
 CC receive percutaneous transluminal coronary angioplasty with an artificial
 CC stent placement.
 XX
 SQ Sequence 5 AA:
 Oy 1 KSKC 5
 Db 1 rpkkc 5
 RESULT 10
 AAB72592
 ID AAB72592 standard; Peptide: 5 AA.
 XX

AC AAB72592;
 XX 09-MAY-2001 (first entry)
 DT Thrombin-induced platelet activator antagonist #31.
 DE Platelet aggregation inhibitor; thrombin activation inhibitor;
 XX protease activated receptor 1; PAR1; platelet activation inhibitor;
 KW thrombosis; acute coronary syndrome.
 KW Unidentified.
 XX WO200112656-A1.
 PN 22-FEB-2001.
 XX 17-AUG-2000; 2000WO-US40669.
 XX 17-AUG-1999; 99US-0375808.
 XX (THRO-) THROMBIN INC.
 PA Schmaier AH, Hasan AAK;
 PI Schmaier AH, Hasan AAK;
 XX WPI; 2001-226546/23.
 DR Inhibiting thrombin activation in human cell expressing protease
 XX activated receptor 1 (PAR1), comprises contacting mixtures of thrombin
 PT and human cell expressing PAR1, with a peptide that inhibits platelet
 PT activation.
 XX Claim 5; Page 25; 49pp; English.
 PS The present invention relates to a method for inhibiting thrombin
 XX activation in a human cell expressing protease activated receptor 1
 CC (PAR1). The method involves using peptides (e.g. the present peptide)
 CC that inhibit platelet activation. The method is useful for preventing
 CC thrombosis and platelet aggregation. The method can be used for patients
 CC with acute coronary syndromes (e.g. crescendo angina, myocardial
 CC infarction) and for individuals who have acute coronary syndromes and
 CC receive percutaneous transluminal coronary angioplasty with an article
 CC stent placement.
 XX Sequence 5 AA;
 SQ

Query Match 59.38; Score 16; DB 22; Length 5;
 Best Local Similarity 40.0%; Pred. No. 3.4e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KSSKC 5
 : :
 Db 1 rgdkc 5

RESULT 11
 AAB37555
 ID AAB37555 standard; peptide; 5 AA.
 XX AAB37555;
 AC 01-MAR-2001 (first entry)
 XX CD8 activation complex RDT ridge analogue SC8-21.
 DT CD8 activation complex; cytotoxic T lymphocyte response; analogue;
 DE surface feature; gene therapy; diabetes; tissue transplantation.
 XX Unidentified.
 OS WO2000066146-A1.
 PN 09-NOV-2000.
 XX

XX 02-MAY-2000; 2000WO-US11902.
 XX 04-MAY-1999; 99US-0132361.
 PR 20-AUG-1999; 99US-0150150.
 PR 01-NOV-1999; 99US-0162632.
 XX (PHIL-) PHILADELPHIA HEALTH & EDUCATION CORP.
 PA Jameson BA, Tretiakova A;
 XX WPI; 2001-015912/02.
 DR Composition for inhibition of detrimental cytotoxic T lymphocyte
 XX responses comprising a compound that mimics or interacts with a surface
 PT feature of the CD8/MHC I complex.
 XX Disclosure; Page 35; 40pp; English.
 PS The present invention provides compositions which can be used to inhibit
 XX detrimental cytotoxic T lymphocyte responses. These compounds mimic or
 CC interact with a surface feature (such as SHN, KIT, SSK, DSK and RDT) of
 CC the CD8/MHCI complex. This is useful in gene therapy, in the treatment of
 CC diabetes and in tissue transplantation.
 XX Sequence 5 AA;
 SQ

Query Match 59.38; Score 16; DB 22; Length 5;
 Best Local Similarity 50.0%; Pred. No. 3.4e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSKC 5
 : :
 Db 2 nnkc 5

RESULT 12
 AAB12055
 ID AAB12055 standard; Peptide; 4 AA.
 XX AAB12055;
 AC 17-JAN-2001 (first entry)
 XX G4 GTPase motif from EF-Tu/ Ha-RAS.
 DE Rb-interacting zinc finger; R12; retinoblastoma; heart disease;
 XX cell proliferation; cell differentiation; tissue repair;
 KW transcription regulator; breast cancer; gene therapy; melanoma;
 KW neuroblastoma; leukaemia; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; paralysis; motor neurone disorder;
 KW G4 GTPase motif; EF-Tu/ Ha-RAS.
 XX Unidentified.
 OS US6069231-A.
 XX 30-MAY-2000.
 PD 18-AUG-1995; 95US-0516859.
 XX 18-AUG-1994; 94US-0292683.
 PR 06-MAR-1995; 95US-0399411.
 XX (LJOL-) LA JOLLA CANCER RES FOUND.
 PA Huang S;
 XX WPI; 2000-410879/35.
 DR New PR domain peptides comprising amino acid sequences from, for
 PT example retinoblastoma-interacting zinc finger, or egl-43 proteins, for

PT *regulating gene transcription and controlling cell proliferation and
 XX differentiation
 PS Disclosure: Column 9; 91pp; English.
 CC The present sequence is a G4 GTPase motif from EF-Ty/ Ha-RAS. The G4
 CC (Rb)-interacting zinc finger (RIZ) protein. RIZ is a nuclear
 CC phosphoprotein that acts as a cell differentiation factor. RIZ can
 CC modulate cell growth by binding to Rb protein, which is involved in
 CC regulating cell proliferation. In addition, RIZ can act to regulate
 CC transcription. RIZ functions to maintain cells in the G1 phase of the
 CC cell cycle. By interacting with Rb through the CR2 domain of RIZ, RIZ
 CC protein is a PR domain protein and is present primarily in the cell
 CC nucleus. RIZ gene mutations may be implicated in various cancers such as
 CC melanoma, neuroblastoma, leukemia and breast cancer, and so the RIZ
 CC gene may be used in gene therapy for these disorders. Since RIZ protein
 CC is implicated in cell cycle arrest, inhibition of RIZ activity may be
 CC useful in neurodegenerative disorder therapy e.g. for Parkinson's,
 CC Huntington's or Alzheimer's disease, paralysis or motor neurone
 CC disorders, or cardiac disorders e.g. heart disease, where the ability to
 CC induce neural/ cardiac tissue proliferation would be useful. The present
 CC sequence was used for sequence homology comparison.
 CC
 CC Sequence 4 AA:
 SQ
 Query Match 55.6%; Score 15; DB 21; Length 4;
 Best Local Similarity 66.7%; Pred. No. 3.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 3 SKC 5
 Db 1 nkc 3
 RESULT 13
 AAY07335
 ID AAY07335 standard; peptide; 5 AA.
 XX
 AC AAY07335;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Matrix metalloprotease inhibitor peptide #6.
 XX
 KW Matrix metalloprotease; inhibitor; tissue damage; angiogenesis; antibody;
 KW arthritis; tumour growth; granulomatous inflammatory condition; enzyme;
 KW metastasis; sarcoidosis.
 XX
 OS Synthetic.
 XX
 PN WO9010228-A.
 XX
 PD 07-SEP-1990.
 XX
 PF 01-MAR-1990; 90WO-US01060.
 XX
 PR 01-MAR-1989; 89US-0317407.
 XX
 PA (USDC) US DEPT OF COMMERCE.
 XX
 PI Krutzsh H, Liotta LA, Stetler-Stevenson W;
 CC WPI; 1990-290458/38.
 DR
 XX
 PT Matrix metallo:proteinase peptide(s) - used to inhibit enzyme in
 PT treating tissue damage caused by activated enzyme
 XX
 XX Claim 3; Page 41; 61pp; English.
 CC This peptide represents a matrix metalloprotease (MMP) inhibitor peptide
 CC of the formula: aal-aa2-aa3-aa4-C where aal and aa4 is R or K; aa2 is K,

CC Q or N; aa3 is P, A, G, L, I or V; and C is a cysteine having a free
 CC sulphydryl group. The peptides can be used to treat tissue damage
 CC caused by activated MMPs, e.g. for treating inappropriate angiogenesis,
 CC arthritis, tumour growth, invasion and metastasis and granulomatous
 CC inflammatory conditions such as sarcoidosis. Antibodies to the peptides
 CC can be used to detect the MMPs and can distinguish activated from latent
 CC enzyme.
 CC
 CC Sequence 5 AA:
 SQ
 Query Match 55.6%; Score 15; DB 11; Length 5;
 Best Local Similarity 40.0%; Pred. No. 3.4e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KSKC 5
 Db 1 kprc 5
 RESULT 14
 AAY07336
 ID AAY07336 standard; peptide; 5 AA.
 XX
 AC AAY07336;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Matrix metalloprotease inhibitor peptide #7.
 XX
 KW Matrix metalloprotease; inhibitor; tissue damage; angiogenesis; antibody;
 KW arthritis; tumour growth; granulomatous inflammatory condition; enzyme;
 KW metastasis; sarcoidosis.
 XX
 OS Synthetic.
 XX
 PN WO9010228-A.
 XX
 PD 07-SEP-1990.
 XX
 PF 01-MAR-1990; 90WO-US01060.
 XX
 PR 01-MAR-1989; 89US-0317407.
 XX
 PA (USDC) US DEPT OF COMMERCE.
 XX
 PI Krutzsh H, Liotta LA, Stetler-Stevenson W;
 CC WPI; 1990-290458/38.
 DR
 XX
 PT Matrix metallo:proteinase peptide(s) - used to inhibit enzyme in
 PT treating tissue damage caused by activated enzyme
 XX
 XX Claim 3; Page 41; 61pp; English.
 CC This peptide represents a matrix metalloprotease (MMP) inhibitor peptide
 CC of the formula: aal-aa2-aa3-aa4-C where aal and aa4 is R or K; aa2 is K,
 CC Q or N; aa3 is P, A, G, L, I or V; and C is a cysteine having a free
 CC sulphydryl group. The peptides can be used to treat tissue damage
 CC caused by activated MMPs, e.g. for treating inappropriate angiogenesis,
 CC arthritis, tumour growth, invasion and metastasis and granulomatous
 CC inflammatory conditions such as sarcoidosis. Antibodies to the peptides
 CC can be used to detect the MMPs and can distinguish activated from latent
 CC enzyme.
 CC
 CC Sequence 5 AA:
 SQ
 Query Match 55.6%; Score 15; DB 11; Length 5;
 Best Local Similarity 40.0%; Pred. No. 3.4e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KSKC 5

Db 1 rpkc 5

RESULT 15

AAR77331
ID AAR77331 standard; Peptide; 5 AA.

XX AC AAR77331;

XX DT 06-FEB-1996 (first entry)

XX DE Human apolipoprotein (a) (apo(a)) antigenic peptide.

XX KW Human; old world monkey; apolipoprotein (a); apo(a); primer; probe;
antigenic peptide; immunoassay; detection; quantification.

XX OS Homo sapiens.

XX PN EP659765-A2.

XX PD 28-JUN-1995.

XX PF 16-DEC-1994; 94EP-0203653.

XX PR 27-JUN-1994; 94US-0266407.

XX PR 21-DEC-1993; 93US-0172461.

XX PA (ALKU) AKZO NOBEL NV.

XX PI Butler SM, Taddei-peters WC;

XX DR WPI; 1995-226203/30.

XX DR N-PSDB; AAQ91625.

XX PT New immuno-reactive peptide(s) of apo:lipoprotein - used for prodn.
of antibodies and development of immunoassays, for the detection and
quantification of apo(a)

XX PS Claim 3; Page 26; 44pp; English.

XX CC AAQ91625 encodes AAR77331 a human/old world monkey apolipoprotein (a)
(apo(a)) antigenic peptide. The peptide can be used to raise anti-
apo(a) antibodies, for use in immunoassays for the detection of
apo(a). The DNA sequence can be used as a primer and/or probe for
the detection, and quantification of apo(a) DNA.

SQ Sequence 5 AA;

Query Match 55.6%; Score 15; DB 16; Length 5;

Best Local Similarity 75.0%; Pred. No. 3.4e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSK 4

Db 1 ksr 4

Search completed: July 19, 2001, 07:50:45
Job time: 166 sec

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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:48:49 : Search time 12.12 Seconds
(without alignments)
8.310 Million cell updates/sec

Title: US-08-487-283A-1_COPY_8_12

Perfect score: 27

Sequence: 1 KSSKC 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 15047

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	66.7	4	1	US-07-694-983-2
2	18	66.7	4	1	US-08-243-082-23
3	15	55.6	4	2	US-08-459-568-41
4	15	55.6	4	2	US-08-399-411-41
5	15	55.6	4	3	US-08-516-859A-41
6	15	55.6	5	1	US-08-363-475-13
7	15	55.6	5	1	US-08-456-840-34
8	15	55.6	5	1	US-08-329-820-102
9	15	55.6	5	1	US-08-329-820-103
10	15	55.6	5	1	US-08-329-820-108
11	15	55.6	5	1	US-08-266-407A-34
12	15	55.6	5	2	US-08-892-544-34
13	15	55.6	5	2	US-08-814-567A-6
14	15	55.6	5	3	US-08-915-189-90
15	15	55.6	5	3	US-08-894-173-36
16	15	55.6	5	4	US-09-398-193-36
17	15	55.6	5	4	US-08-660-092-192
18	14	51.9	3	1	US-07-789-913-26
19	14	51.9	3	1	US-08-049-794-26
20	14	51.9	3	1	US-08-496-847-26
21	14	51.9	3	2	US-08-742-774-26
22	14	51.9	3	2	US-08-675-354-26
23	14	51.9	3	2	US-08-965-918-26
24	14	51.9	3	2	US-09-138-439-26
25	14	51.9	3	3	US-08-613-400A-26
26	14	51.9	3	3	US-09-298-017-26
27	14	51.9	4	4	US-09-392-979A-26

28	14	51.9	4	1	US-07-694-983-3	Sequence 3, Appl1
29	14	51.9	4	1	US-07-694-983-4	Sequence 4, Appl1
30	14	51.9	4	1	US-08-234-602-7	Sequence 7, Appl1
31	14	51.9	4	2	US-08-244-496-5	Sequence 5, Appl1
32	14	51.9	4	2	US-08-244-496-47	Sequence 47, Appl1
33	14	51.9	4	6	5168050-9	Patent No. 5168050
34	14	51.9	5	1	US-08-234-602-8	Sequence 8, Appl1
35	14	51.9	5	1	US-08-199-778-5	Sequence 5, Appl1
36	14	51.9	5	1	US-08-483-434A-35	Sequence 35, Appl1
37	14	51.9	5	2	US-08-244-496-48	Sequence 48, Appl1
38	14	51.9	5	2	US-08-531-525-2	Sequence 22, Appl1
39	14	51.9	5	2	US-08-928-958-72	Sequence 2, Appl1
40	14	51.9	5	2	US-08-718-270A-2	Sequence 168, App
41	14	51.9	5	2	US-08-747-137-168	Sequence 22, Appl1
42	14	51.9	5	2	US-09-072-429-22	Sequence 168, App
43	14	51.9	5	2	US-08-760-903-5	Sequence 5, Appl1
44	14	51.9	5	3	US-08-722-258-71	Sequence 71, Appl1
45	14	51.9	5	4	US-08-882-046-107	Sequence 107, App

ALIGNMENTS

RESULT 1
US-07-694-983-2
; Sequence 2, Application US/07694983
; Patent No. 5432260
; GENERAL INFORMATION:
; APPLICANT: Stahl, Phillip D.
; TITLE OF INVENTION: HIGH AFFINITY MANNOSE RECEPTOR
; NUMBER OF INVENTION: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Irell & Manella
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/694,983
; FILING DATE: 19910503
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9500-0039.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-694-983-2

Query Match 66.7%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 KSSK 4
IIII
Db 1 KSSK 4

RESULT 2
US-08-243-082-23
; Sequence 23, Application US/08243082
; Patent No. 5506120
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Hiroaki
; APPLICANT: YAMASHITA, Kunihiko
; TITLE OF INVENTION: METHOD OF PRODUCING PEPTIDES OR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spencer, Frank & Schneider
; STREET: 1111 Nineteenth Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/243,082
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,754
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Schneller, John W.
; REGISTRATION NUMBER: 26,031
; REFERENCE/DOCKET NUMBER: KOWAT 0010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 828-8000
; TELEFAX: (202) 828-8038
; TELEX: SPENCER 64267
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-243-082-23

Query Match 66.7%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSKK 4
|
|
|
|
Db 1 KSKK 4

RESULT 3
US-08-459-568-41
; Sequence 41, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/459,568
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-41

Query Match 55.6%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
|
|
|
Db 1.NKC 3

RESULT 4
US-08-399-411-41
; Sequence 41, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-399-411-41

Query Match 55.6%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
: 11
DB 1 NKC 3

RESULT 5

US-08-516-859A-41
; Sequence 41, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859A
; FILING DATE: 18-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-516-859A-41

Query Match 55.6%; Score 15; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
: 11
DB 1 NKC 3

RESULT 6

US-08-363-475-13
; Sequence 13, Application US/08363475
; Patent No. 551679
; GENERAL INFORMATION:
; APPLICANT: Chiang, Shu-Jen

APPLICANT: Burnett Jr., William V.
; APPLICANT: Tonzi, Sean M.
; TITLE OF INVENTION: PENICILLIN V AMIDOHYDROLASE GENE FROM
; TITLE OF INVENTION: FUSARIUM OXYSPORUM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas R. Savitsky
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,475
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitsky, Thomas R.
; REGISTRATION NUMBER: 31,661
; REFERENCE/DOCKET NUMBER: ON-0134
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 252 4956
; TELEFAX: (609) 252 4526
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-363-475-13

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
: 11
DB 2 AKC 4

RESULT 7
US-08-456-840-34
; Sequence 34, Application US/08456840
; Patent No. 5597908
; GENERAL INFORMATION:
; APPLICANT: Taddel-Peters, W. C.
; APPLICANT: Butler, Sandra M.
; TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5597908el
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,840
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/266,407
FILING DATE: 27-JUN-1994
APPLICATION NUMBER: US 08/172,461
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELEPHONE: 301-258-5200
TELEFAX: 301-977-0847
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-840-34

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 KSSK 4
Db 1 KSSR 4

RESULT 8
US-08-329-820-102
Sequence 102, Application US/08329820
Patent No. 5747457
GENERAL INFORMATION:
APPLICANT: JONCZYK, ALFRED
APPLICANT: FELDING-HABERMANN, BRUNHILDE
APPLICANT: DIEFENBACH, BEATE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4336758.5
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1635
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /product= "Cys-trityl"
OTHER INFORMATION: /note= "S-trityl"

FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "Lys(BOC)"
OTHER INFORMATION: /note= "N-terminal: FMOC"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /product= "Thr(But)"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "Asp(OBut)"
US-08-329-820-102

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSK 5
Db 1 KTADC 5

RESULT 9
US-08-329-820-103
Sequence 103, Application US/08329820
Patent No. 5747457
GENERAL INFORMATION:
APPLICANT: JONCZYK, ALFRED
APPLICANT: FELDING-HABERMANN, BRUNHILDE
APPLICANT: DIEFENBACH, BEATE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4336758.5
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1635
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /product= "Cys-trityl"
OTHER INFORMATION: /note= "S-trityl"
US-08-329-820-103

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSKC 5
DB 1 KTADC 5

RESULT 10

US-08-329-820-108
Sequence 108, Application US/08329820
Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED
APPLICANT: FELDING-HABERMANN, BRUNHILDE
APPLICANT: DIEFENBACH, BEATE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5
FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /product="Boc-Lys(Boc)"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 2

OTHER INFORMATION: /product="Thr(But)"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: /product="Asp(Obut)"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: /product="Cys(Trt)"

US-08-329-820-108

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 KSSKC 5

DB 1 KTADC 5

RESULT 11

US-08-266-407A-34
Sequence 34, Application US/08266407A
Patent No. 5786156

GENERAL INFORMATION:

APPLICANT: Taddel-Peters, W. C.

APPLICANT: Butler, Sandra M.

TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESSES:

ADDRESSEE: AKZO No. 5786156el

STREET: 1330 Piccard Drive

CITY: Rockville

STATE: Maryland

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,407A
FILING DATE: 27-JUN-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/172,461
FILING DATE: 21-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Gornley, Mary E.

REGISTRATION NUMBER: 34,409

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-258-5200

TELEFAX: 301-977-0847

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-266-407A-34

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSK 4

DB 1 KSSR 4

RESULT 12

US-08-892-544-34

Sequence 34, Application US/08892544
Patent No. 5874544

GENERAL INFORMATION:

APPLICANT: Taddel-Peters, W. C.

APPLICANT: Butler, Sandra M.

TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESSES:

ADDRESSEE: AKZO No. 5874544el

STREET: 1330 Piccard Drive

CITY: Rockville

STATE: Maryland

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/892,544
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/266,407
;; FILING DATE: 27-JUN-1994
;; APPLICATION NUMBER: US 08/172,461
;; FILING DATE: 21-DEC-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gormley, Mary E.
;; REGISTRATION NUMBER: 34,409
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-258-5200
;; TELEFAX: 301-977-0847
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-892-544-34

Query Match 55.6%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSR 4
Db 1 KSSR 4

RESULT 13
US-08-814-567A-6
; Sequence 6, Application US/08814567A
; Patent No. 5998598
; GENERAL INFORMATION:
; APPLICANT: CSARY, KARL G.
; APPLICANT: ANGLADE, EDDY
; APPLICANT: SULLIVAN, DANIEL M.
; APPLICANT: LAROCHELLE, WILLIAM
; TITLE OF INVENTION: IMMUNOADHESINS AND METHODS OF PRODUCTION
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 PEACHTREE STREET, NE
; CITY: ATLANTA
; STATE: GEORGIA
; COUNTRY: USA
; ZIP: 30303-1811
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,567A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: SELBY, ELIZABETH
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 14014.0214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 6:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-814-567A-6

Query Match 55.6%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSK 4
Db 2 KSSR 5

RESULT 14
US-08-915-189-90
; Sequence 90, Application US/08915189
; Patent No. 6001965
; Patent No. 6001965 6001955
; GENERAL INFORMATION:
; APPLICANT: Livant, Donna L.
; TITLE OF INVENTION: Anticancer Compounds and Methods
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,189
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UM-02877
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
;; US-08-915-189-90

Query Match 55.6%; Score 15; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
Db 3 SRC 5

RESULT 15
US-08-894-173-36
; Sequence 36, Application US/08894173A
; Patent No. 6090612

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: GENERAL INFORMATION:
: APPLICANT: Medical Research Council
: TITLE OF INVENTION: Adenylate cyclase and uses therefor
: FILE REFERENCE: P14716C
: CURRENT APPLICATION NUMBER: US/08/894,173A
: CURRENT FILING DATE: 1997-08-13
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 36
: LENGTH: 5
: TYPE: PRT
: ORGANISM: Mouse
: FEATURE:
: OTHER INFORMATION: STRANDEDNESS : Single
: FEATURE:
: OTHER INFORMATION: TOPOLOGY : Linear
: FEATURE:
: OTHER INFORMATION: MOLECULE TYPE : Peptide
: FEATURE:
: OTHER INFORMATION: HYPOTHETICAL : NO
: FEATURE:
: OTHER INFORMATION: ANTI-SENSE : NO
US-08-894-173-36

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Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 3 SKC 5
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Db 1 TKC 3

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Search completed: July 19, 2001, 07:51:04
Job time: 135 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 00:49:32 ; Search time 2123.9 Seconds
(without alignments)
5440.185 Million cell updates/sec

Title: US-08-487-283A-8
Perfect score: 747
Sequence: 1 ATGCCCATATCCAGATGAC.....TGGTCACTGTCTCGAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	310.6	41.6	840	56 AF329458	AF329458 Synthetic
3	294	39.4	819	9 A18692	A18692 Synthetic n
4	290.4	38.9	1637	9 AX006750	AX006750 Sequence
5	283.4	37.9	723	9 AR003797	AR003797 Sequence
6	283.4	37.9	723	9 AR010133	AR010133 Sequence
7	283.4	37.9	723	9 AR055339	AR055339 Sequence
8	283.4	37.9	723	10 I11980	I11980 Sequence 92

9	283.4	37.9	723	10	I40550	I40550 Sequence 89
10	266	35.6	2871	9	AX023363	AX023363 Sequence
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12	259	34.7	1630	9	AX023365	AX023365 Sequence
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15	250	33.5	729	9	AR027053	AR027053 Sequence
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18	249.2	33.4	780	56	SYNN198SCF	SYNN198SCF Synthetic s
19	247.2	33.1	916	10	I45604	I45604 Sequence 29
20	245.6	32.9	828	94	NM295478	NM295478 Mus muscul
21	245.2	32.8	1371	9	AX023359	AX023359 Sequence
22	245.2	32.8	1389	9	AX023361	AX023361 Sequence
23	242	32.4	1611	9	AX014270	AX014270 Sequence
24	241.6	32.3	877	10	E31225	E31225 Device for
25	241.6	32.3	925	10	E30616	E30616 Antibody an
26	239.6	32.1	1149	9	G3778	G3778 Sequence 42
27	239.6	32.1	1212	9	A63772	A63772 Sequence 36
28	239.6	32.1	1422	9	G3768	G3768 Sequence 32
29	239.6	32.1	1545	9	A63770	A63770 Sequence 34
30	239.6	32.1	1956	9	A63774	A63774 Sequence 38
31	239.6	32.1	2079	9	A63776	A63776 Sequence 40
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35	236.6	31.7	733	9	AR088764	AR088764 Sequence
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37	234.4	31.4	721	9	AR088763	AR088763 Sequence
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43	231	30.9	6727	9	AR074430	AR074430 Sequence
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ALIGNMENTS

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DEFINITION Streptomyces avidinii.
ACCESSION  AX057943
VERSION    AX057943.1
KEYWORDS   GI:12310570
SOURCE     Streptomyces avidinii.
ORGANISM   Streptomyces avidinii
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE  1 (bases 1 to 1612)
AUTHORS   Goshorn,S.C., Graves,S.S., Schultz,J.E., Lin,Y., Sanderson,J.A. and
            Reno,J.M.
TITLE      Streptavidin expressed gene fusions and methods of use thereof
JOURNAL    Patent: WO 0075333-A 3 14-DEC-2000;
            NEORX CORPORATION (US)
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Matches 489; Conservative 0; Mismatches 242; Indels 9; Gaps 2;
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/db.xref="GI:513359"
/translational="KMKRTAIAIVALAGFATVAQADIQMTQSPASLSVSNGEYVITIT
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EDGSGYCOHFHWGPTPYFGGCTKLEIRFGSGSGSGSGGSGVOQLQDSPAELVFKG
ASYKSCASGAYPTFDHAIHAKOKPDEGLMIGIYISPGNDIKENLEPKRATITLAD
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[illegible]

Query Match 37.9%; Score 283.4; DB 9; Length 723;
Best Local Similarity 63.7%; Pred. No. 9.1e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

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Db 61 ATCATTCTGCGGGGCGAGTACAGACATTAATAGCTATTTAAGCTGGTCCAGCAGAACCA 120
OY 127 GGGAAAGCTCCGAGCTCTGATTTACGGTGCAGCAACCTGCAGATGAGTCCCTCT 186
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Db 121 GGGAAAGCTCTTAAGACCCCTGATCTATCGTGAACAGATTTGGAATCTGGGGTCCCATCA 180
OY 187 CGCTTCTGTGATCCGGCTCCGGAACGGATTTTACTCTGACCATTCAGCACTCTGACGCT 246
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Db 595 AACACTGCTATTTACATCAACACGCTCAGAGCGAGACAGCGCTGTGTAATTTCTGT 654
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RESULT 6
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LOCUS AR010133
DEFINITION Sequence 89 from patent US 5756699.
ACCESSION AR010133
VERSION AR010133.1 GI:3968938
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 723)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5756699-A 89 26-MAY-1998;
FEATURES
SOURCE Location/Qualifiers
1..723
BASE COUNT 178 a 162 c 207 g 176 t
ORIGIN

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Query Match 37.9%; Score 283.4; DB 9; Length 723;
 Best Local Similarity 63.7%; Pred. No. 9,1e-71;
 Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

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OY 7 GATATCCAGATGACCCATCCCCGCTCCCTGTCCGCGCTCTGTGGGGATAGGCTACC 66
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Db 1 GACATCCCAATGACCTAGCTCCATCTCCCTGCTGCACTCTAGAGACAGATCACT 60
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Db 355 GGTGGAGGATCTGAGATCCAGTGTGTGTCAGTGTGAGAGAGGCTGTGTAAGGCTGGAAGG 414
OY 427 TCAGTCAAGTGTCCGTGTAAGCTAGCGGCTATATTTTCTTAATTAATTTGATTTCAATGG 486
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ACCESSION AR055339
VERSION AR055339.1 GI:5980916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 723)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Polynucleotides encoding gelonin sequences
JOURNAL Patent: US 5837491-A 89 17-NOV-1998;

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Best Local Similarity 63.7%; Pred. No. 9.1e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;
QY 7 GATATCCAGATGACCCAGTCCCTCCCTGTCGCGCTCTGTGGCGATAGGCTCACC 66
DB 1 GACATCCAGATGACTCAGTCTCCATCTCCCTGTCGATCTGTAGGACAGAGTCACT 60
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QY 607 AGTACAGTATACATGAGCTCTCCAGCTCGATCGGAGGACACCGCGCTCTATTATTCG 666
DB 595 AACACTGCCTATTTACAGATCAACAGCCTCAGAGCCGAGGACACCGCTGTGTTCTGT 654
QY 667 GCGGTTATTTTGGTTCTAGCCGAAATGGTATTTGGTATTTGGGTTCAAGGAACC 726
DB 655 ACAGACGGGGTTACG -----ACTGGTACTTCGATGCTGGGGCCAGGGACC 702
QY 727 CTGCTCACTGTCTCGAGCTGA 747
DB 703 ACGGTCACCGTCTCCTCATGA 723

RESULT 8
111980
LOCUS 111980 723 bp DNA PAT 26-JUL-1995
DEFINITION Sequence 92 from Patent US 5416202.
ACCESSION 111980
VERSION 111980.1 GI:909423
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 723)
REFERENCE Bernhardt, S.L., Better, M.D., Carroll, S.F., Lane, J.A. and Lei, S.
AUTHORS Materials comprising and methods of preparation and use for
TITLE Ribosome-inactivating proteins
JOURNAL Patent: US 5416202-A 92 16-MAY-1995;
FEATURES Location/Qualifiers
1. .723
BASE COUNT 178 a 162 c 207 g 176 t
ORIGIN
Query Match 37.9%; Score 283.4; DB 10; Length 723;
Best Local Similarity 63.7%; Pred. No. 9.1e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;
QY 7 GATATCCAGATGACCCAGTCCCTCCCTGTCGCGCTCTGTGGCGATAGGCTCACC 66
DB 1 GACATCCAGATGACTCAGTCTCCATCTCCCTGTCGATCTGTAGGACAGAGTCACT 60
QY 67 ATCACTTCGGCGCCAGCGAAACATCTATGGCGCTGAACTGCTATCAACGTAACCT 126
DB 61 ATCACTTCGGCGCGAGTCAGGACATTAATAGCTATTAAAGCTGGTCCAGCAGAAACCA 120
QY 127 GGGAAAGCTCCGAAGCTTCTGATTTACGGTGGCGAAGCTGGCAGATGGAGTCCCTTCT 186
DB 121 GGGAAAGCTCCTAGACCTGATCTATCTGTCGAACAGATTGGAACTGGGGTCCCATCA 180
QY 187 CGCTTCTCTGATCCGGTCCGGAACGATTTCACTCTGACCATCAGCAGTCTGCAGCCT 246
DB 181 AGGTTCACTGAGTGGATCTGGGACAGATTATATCTCTCACCATCAGCAGCCTGCAATAT 240
QY 247 GAAGCTTCCTAGCTATTAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 306
DB 241 GAAGCTTCCTAGCTATTAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 300
QY 307 GGTACCAAGTGGAAATAAACAGTCTGCGGCTGGTGGTCTGTCGCGGTGGATCTGGT 366
DB 301 GGTACCAAGTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 354
QY 367 GGTGGCGGTTCTCAAGTCCCACTGGTGCATCCGCGCCGAGGTCAAGAAGCCAGGGGCC 426
DB 355 GGTGGAGGATCTGAGTCCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 414
QY 427 TCAGTCAAGTGTCTTCAAGTCCCACTGGTGCATCCGCGCCGAGGTCAAGAAGCCAGGGGCC 486
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QY 487 GTGCGTCAGGCGCCCGGCGAGGCTGGAATGGATGGTGGTGGATCTTACCGGCTCTGGT 546
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DB 595 AACACTGCCTATTTACAGATCAACAGCCTCAGAGCCGAGGACACCGCTGTGTTCTGT 654
QY 667 GCGGTTATTTTGGTTCTAGCCGAAATGGTATTTGGTATTTGGGTTCAAGGAACC 726
DB 655 ACAGACGGGGTTACG -----ACTGGTACTTCGATGCTGGGGCCAGGGACC 702
QY 727 CTGCTCACTGTCTCGAGCTGA 747
DB 703 ACGGTCACCGTCTCCTCATGA 723

RESULT 9
140550
LOCUS 140550 723 bp DNA PAT 13-MAY-1997

DEFINITION	Sequence 89 from patent US 5621083.
ACCESSION	140550
VERSION	140550.1
KEYWORDS	GI:2082842
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 723)
AUTHORS	Better,M.D., Carroli,S.F. and Studnicka,G.M.
TITLE	Immunotoxins comprising ribosome-inactivating proteins
JOURNAL	Patent: US 5621083-A 89 15-Apr-1997;
FEATURES	Location/Qualifiers
source	1..723
BASE COUNT	178 a 162 c 207 g 176 t
ORIGIN	
Query Match	37.9%; Score 283.4; DB 10; Length 723;
Best Local Similarity	63.7%; Pred. No. 9.1e-71;
Matches 472; Conservative	0; Mismatches 251; Indels 18; Gaps 2;
QY	7 GATATCCAGATGACCCAGTCCCGCTCCTCCCTGTCGCGCTCTGTGGCGATAGGCTACCC 66
Db	1 GACATCCAGATGACATCATCTCCATCTCCCTGCTGCTCATCTGTAGGAGACAGATCACT 60
QY	67 ATCACCTCCGGCGCCGACGGAACACATCTATGGCGCGCTGACACTGGTATCACTAACT 126
Db	61 ATCACTTCCCGGGCCAGTCAGACACTTAATACCTATTTAAAGCTGGTCCAGCAAAACCA 120
QY	127 GGGAAAGTCCGAACCTCTGTATTCAGGTGGAGCAACCTGGCAGATGGATCCCTCT 186
Db	121 GGGAAAGTCCCTAAGACCTTATCTATGTGTGCAAAACAGATTGGAAATCTGGGTCCATCA 180
QY	187 CGCTTCTCGATCCGGCTCCGGAAAGGATTTACCTGACCATCAGCAGTCTGACGCT 246
Db	181 AGGTTCACTGGCAGATGGAGATCTGGACAGATATATCTCACCATCAGCAGCTCGCAATAT 240
QY	247 GAAGACTTCGCTACCTATTACTGTAGAACGTTTAAATACTCCGTTGACTTTGGACAG 306
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Db	415 TCCGCAAAATCTCTCGCGACGCTCTGGGTATACCTTCACAACTATAGATGAAGTGA 474
QY	487 GTGGCTCAGGGCCCCGGGACAGGGCTTGGAAATGATGGGTGAGATCTTACCGGGCTCTGCT 546
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QY	547 AGCACCCGAATTAACGAAATTTTAAACAGCCGTGTATATGATGACGCGTACACTCGACT 606
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QY	607 AGTACAGTATACATGAGAGCTCTCAGCCCTGGATCGAGAGACAGCGCGCTCATTTATTGC 666
Db	595 AATCACTGCTATTTACAGATCAACAGCGCTCAGAGCGGAGACACGCGCTGTATTTCTGT 654
QY	667 GCGCGTATTTTGTGTTCTAGCCCGAATTGGTATTTTGTATGTTTGGGCTCAAGAAC 726
Db	655 ACAAGACGGGGTTACG-----ACTGTACTTCGATGTCGTGGGGCCCAAGGAGCC 702
QY	727 CTGGCTACTGTCTGAGCTGA 747
Db	703 ACGGTCACCGTCTCTCATGA 723

[illegible]

Db 790 TATGTATGACTACTGGGTCAGGAACCTCAGTCACCTCTC 833

RESULT 12

AX023365

LOCUS AX023365 1630 bp DNA PAT 15-SEP-2000

DEFINITION Sequence 36 from Patent W00006605.

ACCESSION AX023365

VERSION AX023365.1 GI:10183777

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1630)

AUTHORS Kufer,P., Zetli,F., Dreier,T., Baeuerle,P.A. and Borschert,K.

TITLE Heteromindbodies

JOURNAL Patent: WO 0006605-A 36 10-FEB-2000;

KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ; BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER BIOMEDIZINIS (DE)

FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

39..1610

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BASE COUNT 376 a 484 c 437 g 333 t

ORIGIN

Query Match 34.7%; Score 259; DB 9; Length 1630;

Best Local Similarity 63.0%; Pred. No. 9.7e-64;

Matches 419; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

Db 448 GCGGCGGGGCTCAGAGGTGCGCTCGAGTCTGGGGAGCGCTGTCAGCCTGGGA 507

Db 425 CCTCAGTAAAGTCTCCGTGTAAGCTAGCGGCTATATTTTCTATATTTGATTCAT 484

Db 508 GGTCCCTAGACTCTCTCTGTCAGCCTCTGATACCTTCAGTACATGACGACT 567

Db 485 GGGTCGTCAGGCCCCGGGCGGCTGGATGGATGGGAGATCTTACCGGGCTCG 544

Db 568 GGGTCGTCAGGCCCCGGGCGGCTGGATGGATGGGAGATCTTATATATATGATGGA 627

Db 545 GTAGCAGCAATATATCCGAATTTTAAAGACCGTGTACTATGACCGCTGACCTGCA 604

Db 628 GTAATAATATATATGACAGCTCCGTAAGGCGCATTCACATCTCCAGACGATTCGA 687

Db 605 CTAGTACAGTATATGAGAGCTCTCAGCTCGATCGGAGGACACGCGCTATATAT 664

Db 688 AGAACACCGCTGATCTGGAATATGACAGCCTGAGAGCTGAGACACGCGCTGATTA 747

Db 665 GCGCG 669

Db 748 GTGCG 752

RESULT 13

AX023367

LOCUS AX023367 1630 bp DNA PAT 15-SEP-2000

DEFINITION Sequence 38 from Patent W00006605.

ACCESSION AX023367

VERSION AX023367.1 GI:10183779

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1630)

AUTHORS Kufer,P., Zetli,F., Dreier,T., Baeuerle,P.A. and Borschert,K.

TITLE Heteromindbodies

JOURNAL Patent: WO 0006605-A 38 10-FEB-2000;

KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ; BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER BIOMEDIZINIS (DE)

FEATURES

source Location/Qualifiers

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39..1613

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BASE COUNT 445 a 410 c 408 g 367 t

ORIGIN

Query Match 34.7%; Score 259; DB 9; Length 1630;

Best Local Similarity 63.0%; Pred. No. 9.7e-64;

Matches 419; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

Qy	65	CCATCACCCTGGGGCCAGCGAAACATCTATGCGCGCTGAACCTGGTATCAACGTAAC	124
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Qy	125	CTGGAAAGCTCCGAGGCTTCTGATTACGCTGCGACGACCTGCGAGTACGAGTCCCTT	184
Db	214	CAGGACAGCTCCAAAGCTGCTCAATTTACTGGGCATCTACCGGGAATCCGGGGTCCCTG	273
Qy	185	CTCGCTTCTCTGGATCCCGCTCCGGAAGGATTTCACTCTGACCATCAGCAGTCTCGACG	244
Db	274	ACCATTCAGCGGCGAGTGAATCTGGGCAAAATACATCTCCACATCAGCAGCTTCGACG	333
Qy	245	CTGAAGACTTCGCTACGATTTACTGTCTGAGAACGTTTTAAATACTCCGTGACTTTTCGAC	304
Db	334	CTGAAGATTTTGGCTACTTACTTTTGTCAACAGTCTGACAGTTTGGCGATCACTTCGGGC	393
Qy	305	AGGCTACCAAGTGGAAATAAAGCTACTTGGCGGTGGTGGTCTGGTGGCGGTGATCTG	364
Db	394	AAGGACACGACTGGACATTCAA-----GGAGGAGGAGGATCAGGTGGTGGTAGCG	447
Qy	365	GTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAGCCAGGG	424
Db	448	CGCGGGGCTCAGAGTGCAGCTGCTCGAGTCTGGGGAGGCGTGTCCAGCCTGGGA	507
Qy	425	CCTCAGTCAAGTGTCTGTAAAGTAGCGGCTATATTTTCTAATTAATTTGATTCAT	484
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Qy	485	GGGTGGCTCAGCCCCCGGCGAGGCTTGGATGATGGTGAGATCTTACCGGCTCTG	544
Db	568	GGGTCCGCGAGGCTCCAGGCAAGGCGTGGAGTGGTGCGAGTTATCATATGATGGAA	627
Qy	545	GTAGCAGCGAATACCCGAAATTTTAAAGACCGTGTACTATGACGCTGACACTTCA	604
Db	628	GTAATAATATATCCAGACTCCCGTGAAGGCGGATTCACATCTCCAGAGCAATCCA	687
Qy	605	CTAGTACAGTATACATGAGGCTCTCCAGCTCGGATCGGAGGACACGCGCTATTAT	664
Db	688	AGAACACGCTGTATCGCAATGAACGCTGAGAGCTGAGGACACGCGTGTGTATTACT	747
Qy	665	GC GCG 669	
Db	748	GTGCG 752	
RESULT	14		
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LOCUS	XXU49832	902 bp	mRNA
DEFINITION	Synthetic single chain Fv antibody against potato virus V coat protein, mRNA, partial cds.	SYN	24-MAR-1996
ACCESSION	U49832		
VERSION	U49832.1	GI:1236090	
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct		
ORGANISM	artificial sequence.		
REFERENCE	1 (bases 1 to 902)		
AUTHORS	Chen,Z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.		
TITLE	Cytoplasmic accumulation of a soluble functional scfv protein to a plant virus expressed as a thioredoxin fusion in Escherichia coli		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 902)		
AUTHORS	Chen,Z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-FEB-1996) 2 C. Chen, Botany, Univ. of Leicester, University Road, Leicester LE1 7RH, UK		
FEATURES	Location/Qualifiers		
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ORIGIN																																																																																																											
Query Match		34.6%;		Score 258.6;		DB 56;		Length 902;																																																																																																			
Best Local Similarity		61.4%;		Pred. No. 1.3e-63;																																																																																																							
Matches 482;		Conservative 0;		Mismatches 249;		Indels 54;		Gaps 2;																																																																																																			
Qy	1	ATGGCGGATATCCAGATGACCCAGTCCCGCTCCCTCCCTCCCGCTCTGTGGCGGATAGG	60	Db	10	ATGGCAGACGTCAGATAATCCAGACTACAGCCCTCCCTATCTGCATCTGTGGGAGAACT	69	Qy	61	GTCCACCATCAGCTGTGGCGCCAGGAAACATCTATGTGGCGCGTGAACCTGGTATCAACGT	120	Db	70	GTCCACCATCAGATGTGAGCAAGTAGGACATATTTACAGTTATTTAGCATGGTATCAGCAG	129	Qy	121	AAACCTGGGAAGCTCCGAAGCTTCTGATTACGGTSCGACGACCTGGCAGATGGAGTC	180	Db	130	AAACGGGAAATCTCTCAGCTCCCTGCTATAGTCAAAAACCTTAGCAGAAGGTGTG	189	Qy	181	CVTTCGCTTCTCTGGATCCGCGTCCGGAACGATTCTACTCTGACCATCAGCAGCTG	240	Db	190	CCATCAAGGTTTCACTGSCAGTGGATCAGGCACACAGTTTCTCTTAAGATCAACAGCCTG	249	Qy	241	CAGCCTGAAGACTTCGCTAGTATTTACTGTGCAACGCTTTTAAATATCTCGTGTGACTTTC	300	Db	250	CAGCCTGAAGATTTTGGAGATTACTGTCAACATCATTTATGATATCTCTCGACGCTTC	309	Qy	301	GGACGGGTACCAAGTGGGAATTAACGTAATCT-----	333	Db	310	GGTGGAGGCACCAAGCTGGAAATCAGACGGGCTGATGCTGCACCAACTGTATCCATCTTC	369	Qy	334	-----GGCGGTGGTGTCTGCTGGTGGCGGTGGATCTGGTGGTGGCGGT	375	Db	370	CCACCATCCAGTCCCGGGGCGGTGGCGGTCTGCTGGCGGTGGCTCTGGCGGTGGCGGT	429	Qy	376	TCCTCAAGTCCAAGTGTGCAATCCGCGCGCAGGTCAGAAGCCAGGGGCTCAGTCAAA	435	Db	430	TCGTGCGACCCAGGTGCGACGAGCTGGGGCTGAGCTGGTGGTCTGGGGCTCAGTGAAG	489	Qy	436	GTGCTCTGTAAAGCTAGCGGCTATATTTTCTAATTTATTTGGATTTCAATGGTGGCTCAG	495	Db	490	ATGCTCTGCAAGGCTTCTGGCTACACATTTACCAGTTTACAAATATGCACTGGGTAAAGCAG	549	Qy	496	GCCCCGGGCGAGGCGCTGGAATGGATGGGTGAGATCTTACCGGGCTCTGTAGCACCGAA	555	Db	550	ACACCTGGACAGGCGCTGGAATGGATGGATGATATTTATCTCGGAATGGTGTACTATC	609	Qy	556	TATACCGGAAATTTTAAAGACCGGTGTACTATGACGCGCTGCACACTTCGACTAGTACAGTA	615	Db	610	TACAATCAGAAGTTCAAGGGCAAGGCCACATTTGACTGCAGACACACATCTCCAGCACAGCC	669	Qy	616	TACATGAGCTCTCCAGCCTCGATCGGAGGACACGCGGCTCTATTTATTCGCGCGGTAT	675	Db	670	AACATCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG	729	Qy	676	TTTTTTGGTCTAGCCCGAATTTGATTTTGGTGGTTCAGGAACTCCCTGGTCACT	735	Db	730	GACTATAG-----GAACACCGCCCTTTGACTTTTGGGGCCAAAGGCACCACTCTCACA	780	Qy	736	GTCTC 740	

Db 781 GNCCTC 785

RESULT 15

AR027053 729 bp DNA

LOCUS AR027053 Sequence 3 from patent US 5856140.

ACCESSION AR027053

VERSION AR027053.1 GI:5937893

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

PAT 29-SEP-1999

1 (bases 1 to 729)
Shimamura,T., Hamuro,J., Nakazawa,H., Kanayama,Y., Sugamura,K. and
Takeshita,T.
gamma-chain human interleukin-2 receptor polypeptide and method of
making
Patent: US 5856140-A 3 05-JAN-1999;
Location/Qualifiers
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Query Match 33.5%; Score 250; DB 9; Length 729;

Best Local Similarity 60.9%; Pred. No. 3.9e-61;

Matches 447; Conservative 0; Mismatches 275; Indels 12; Gaps 2;

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DB 64 ATCACCCTGGCGCCGCGAAACATCTATGCGCGCTGAACGTATCAAGTAAACT 123
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OY 187 CGCTTCTCTGATCCGCTCCGAGAGGATTTGACATCTGACAGTCTGACGCT 246
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OY 307 GGTACCAAGGTGGAATTAAGCTTACTGGCGGTGCTGCTGCTGCTGCTGCTGCT 366
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OY 487 GTGCGTCAGGCGCGCGAGGCTGGAATGAGTGGTGAATCTTACCGGCTGTGT 546
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OY 607 AGTACAGTATACAGCTCTCCAGCTGCGATCGGAGACAGAGCGCTGTATTTGCTC 666
DB 595 ACCACAGCTTACATGAGCTCCACAGCTGACATCTGAGAGCTCTGAGTCTATTTACTGT 654

OY 667 GCGGCTATTTTGTGTTCTAGCCGAATGCTATTTGATGTTGGGCTCAGGAAAC 726
DB 655 GCAAGAGAAATTAATTAAGCTAGGAGTACGAGTACGAGTACGAGTACGAGT 711
OY 727 CTGCTACTGCTCTC 740
DB 712 CTGCTACTGCTCTC 725

Search completed: July 20, 2001, 02:33:26
Job time: 6234 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 00:48:12 ; Search time 1948.2 Seconds
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Title: US-08-487-283A-8
Perfect score: 747
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
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Post-processing: Minimum Match 08
Maximum Match 1008
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	194.2	26.0	422	115	AM407904	AM407904 UI-HF-BL0
2	189.4	25.4	493	115	AM405753	AM405753 UI-HF-BL0
3	188.8	25.3	480	32	AV733319	AV733319 AV733319
4	186.2	24.9	487	115	AM405301	AM405301 UI-HF-BL0
5	184.6	24.7	471	115	AM406294	AM406294 UI-HF-BL0
6	184.6	24.7	566	115	AM406081	AM406081 UI-HF-BL0
7	184.6	24.7	864	155	BG548281	BG548281 602575248
8	184.6	24.7	957	152	BG341934	BG341934 602463276
9	184.6	24.7	959	152	BG341941	BG341941 602463283
10	183.2	24.5	608	115	AM404714	AM404714 UI-HF-BL0
11	183.2	24.5	431	115	AM406886	AM406886 UI-HF-BL0
12	183.2	24.5	447	115	AM405752	AM405752 UI-HF-BL0
13	183.2	24.5	460	115	AM405906	AM405906 UI-HF-BL0
14	182.8	24.5	653	115	AM391263	AM391263 OV0-ST021
15	181.6	24.3	867	155	BG539961	BG539961 602567476
16	179.8	24.1	391	115	AM404992	AM404992 UI-HF-BL0
17	179.8	24.1	453	115	AM383563	AM383563 PM4-HT034
18	179.8	24.1	1135	172	BP975451	BP975451 602245984
19	179.4	24.0	488	115	AM403591	AM403591 UI-HF-BK0
20	178.2	23.9	555	32	AV682898	AV682898 AV682898
21	178.2	23.9	668	32	AV688963	AV688963 AV688963
22	178.2	23.9	671	32	AV712126	AV712126 AV712126
23	178.2	23.9	671	155	BG537798	BG537798 602566152
24	178.2	23.9	675	32	AV696032	AV696032 AV696032
25	178.2	23.9	676	32	AV696029	AV696029 AV696029
26	178.2	23.9	706	32	AV682465	AV682465 AV682465
27	178.2	23.9	768	32	AV695127	AV695127 AV695127
28	177.4	23.7	857	155	BG540224	BG540224 602569113
29	177.4	23.7	921	152	BG341239	BG341239 602463904
30	176.8	23.7	872	154	BG535392	BG535392 602563053
31	176.8	23.7	927	155	BG536845	BG536845 602566383
32	176.6	23.6	426	115	AM405900	AM405900 UI-HF-BL0
33	176.6	23.6	466	115	AM406828	AM406828 UI-HF-BL0
34	176.6	23.6	855	154	BG506654	BG506654 601861253
35	176.6	23.6	992	172	BP976253	BP976253 602245130
36	175.2	23.5	413	5	AA301347	AA301347 EST14279
37	175.2	23.5	444	32	AV686883	AV686883 AV686883
38	175.2	23.5	724	155	BG537031	BG537031 602565115
39	175	23.4	418	115	AM404507	AM404507 UI-HF-BL0
40	175	23.4	655	155	BG569796	BG569796 602590416
41	175	23.4	891	155	BG540787	BG540787 602570674
42	175	23.4	935	152	BG342083	BG342083 602463029
43	175	23.4	972	155	BG545480	BG545480 602572716
44	175	23.4	1130	151	BF662874	BF662874 602144820
45	175	23.4	1198	151	BF663671	BF663671 602145380

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.	1	(bases 1 to 422)	NIH-MGC http://mgi.nci.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
	AM407904	1 GI:6926961	EST.				human.					
	AM407904	422 bp mRNA	EST	16-FEB-2000	UI-HF-BL0-add-a-01-0-ui.r2 NIH_MGC_37 Homo sapiens cDNA clone	IMAGE:3061128 5', mRNA sequence.	human.					
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Email: cgabps-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbnp/image/image.html
 Seq primer: m13 forward

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/cell_line="MGC85"
/lab_host="DH10B (UT1)"
/note="Vector: pRTT3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staedt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
128.C 116.G 121.B

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BASE COUNT	122 a	128 c	116 g	121 t
ORIGIN				

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Best Local Similarity	71.4%;	Pred. No. 8.9e-47;		
Matches 245; Conservative	0;	Mismatches 98;	Indels 0;	Gaps 0;

OY	7	GATATCCAGATGACCAAGCTGCCCGCCTCCCTGCCTGGCCTGTGGGGCATPAGGGTACC	66
Db	42	GACATCCAGATGACCAAGCTGCCCGCCTCCCTGCCTGTGGAGACAGAGTACC	101
OY	67	ATCACCTGCGCGCGCCAGCAAAATCATTTATGGCGCGCTGAACCTGGTATCAACGTAACCT	128
Db	102	ATCACCTGCGCGCGCAATTCAGAGATTATGACAGCATTTAATTGGTATCAGCAGAACA	161
OY	127	GGGAAAGCTCCGAGCTTCGTGATTTACGGTGCGAGCAACTGGCAGATGAGTCCCTTC	188
Db	162	GGGAAAGCCCCCTATCTCTGATTTATGTTGCAATCCATTTGGCAAATGGGGTCCATCA	221
OY	187	CGCTTCTCTGATCCGGCTCCGGAACGGATTTACTGTGACATCAGCACTCTGCACT	248
Db	222	AGCTTACGTGCACTGGATCTGGGACAGATTTTCACTCTCAACATCAGCACTGTCAACT	281
OY	247	GAAACCTTCGTACGTATTACTGCACAAAGCTTTTAATFACCGGTGACTTTGGACAG	306
Db	282	GAAATATTTGGAACTTACTACTGTCAACAGAGTTACAGTGCCTCCCTGACAGTTTTGGCCAG	341
OY	307	GGTCCCAAGGTGAAAATAAAACGTACGGGGGTGTTGGTCTG	349
Db	342	GGGACCAAGCTAGAGATCAAAAGCAACTGTGGTCCACTCATCTG	384

[illegible]JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E Consortium/LLNL at: www.bio.llnl.gov/db/ftp/image/image.html
seq primer: M3 forward.

FEATURES	Location/Qualifiers
source	1. .471

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/db_xref="taxon:9606"
/clone="IMAGE:3059657"
/clone_lib="NH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (UT)"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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BASE COUNT	115 a	132 c	110 g	114 t
ORIGIN				

Query Match	24.7%;	Score 184.6;	DB 115;	Length 471;
Best Local Similarity	71.1%;	Pred. No. 2.8e-46;		
Matches 244;	Conservative	0;	Mismatches 99;	Indels 0;
			Gaps	0;

Qy	7	GATATCCGATGATACCAGTATCCCGCTGCTCCCTGTGTCGCGCTGTGTGGGATAGGGTATACC	66
Db	57	GACATCTCCAAATGACCACCACTGTCCATCTCCCTGCTGTGATGTAGGGAGACAGATATACC	116
Qy	67	ATTCACCTCCGGCCGACAGGAATAATCTATGGCGGCTGAATCTGGTATCAACGTAAACT	126
Db	117	ATTCACCTTGGCCGGACACAGTCACAGCATTTAGAACCTATTTAAATTTGGTATCAGCAAAAACA	176
Qy	127	GGGAAAGCTCCGGAAGCTTCTGATTTACGGTCGAGCAAACTGGCAGATGGAGTCCCTTC	186
Db	177	GGGAAAGCCCTTAACCTGCTATCTATGCTCTGCATTCACATTTGGCAAAATGGGGGTCCATCA	236
Qy	187	CGCTTCTCTGTGATCCGGCTCCGGAACGGATTTCACTGTGACATATCAGCATGTCTCAACCT	246
Db	237	AGGTTCACTGTCAGTGTGATCTGGGACACATTTCACTCTCACCATCAGCATGTCTCAACCT	296
Qy	247	GAAAGACTTCGCTACGTATTTACTGTGCAGACGTTTTAAATACTCCGTTGACTTTTGGGACAG	306
Db	297	GAAATATTTTGCACCTACTACTGTGCACAGAGTTACATACATACCCTGTGACGTTTGGGCCAA	356
Qy	307	GGTACCAAGGTGGAATPAACAGTACTGCGGCTGGTGGTTCTG	349
Db	357	GGGACCAAGGTGGAATPAACAGAACTGTGGCTGCACCATCTG	399

RESULT	6
AM406081	
LOCUS	AM406081 566 bp mRNA EST 16-FEB-2000
DEFINITION	U1-HF-BLO-acv-h-03-0-U1.r1 NH_MGC_37 Homo sapiens cDNA clone IMAGE:3060700 5', mRNA sequence.
ACCESSION	AM406081
VERSION	AM406081.1 GI:6925102
KEYWORDS	- EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 566)

	KEYWORDS	EST .
	SOURCE	human.
	ORGANISM	Homo sapiens
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	TITLE	1 (bases 1 to 957)
	JOURNAL	NIH-MGC http://mgc.nci.nih.gov//.
	COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1998)
		Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://lmcg.lnl.gov Plate: LCM1288 row: g column: 19 High quality sequence stop: 673.
	FEATURES	Location/Qualifiers
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		/clone="IMAGE:4576170"
		/clone_lib="NIH_MGC_48"
		/tissue_type="Primary B-cells from tonsils (cell line)"
		/lab_host="DH10B (phage-resistant)"
		/note="Organ: B-cells; Vector: pORF7; Site.1: XhoI; Site.2: EcoRI; cDNA made by oligo-dT priming, directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGCAGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
BASE COUNT	242 a	266 c 231 g 217 t 1 others
ORIGIN		
Query Match	24.7%	Score 184.6; DB 152; Length 957;
Best Local Similarity	71.1%;	Pred. NO.3.4e-46;
Matches 244; Conservative	0; Mismatches 99; Indels	0; Gaps 0;
OY	7	GATATCCAGATTACGCCCGCTGCTCCCTGTCCGCTGTGGGCGATAGGTTACC 66
Db	53	GACTTCGAGATGAACCATCAATGCTTCACCTCCCTGCTGATGTGAGACAGACTCAC 112
OY	67	ATCACCTGGGGCGCCAGCGAATAATCTATGCGCGCTGAACTGTAACGTAACCT 126
Db	113	ATCACTTGCGGGCGACGATCAGGCAATTAACAATTTTTTAGCTGGTATCAGCAAACHA 172
OY	127	GGGAAAGCTCCGAACCTCTGATTAAGGTGGAGAACCTGGCAGAATGAGATCCCTTCT 186
Db	173	GGGAAAGTTCCTAACCTCCTGATCTATGCTGATCCACTTTGCAATCAGGGGCTCCATCT 232
OY	187	GCGTTCTCTGATCCGGCTCCGGAACGAGTTCACCTGTGACCATAGCAGAGTGGAGCT 246
Db	233	CAGTTCAAGTGGAGAGGCTCTGGAGACAGATTTCACTCTCAGCATAGCAGCTCGAGCT 292
OY	247	GAAAGCTTCGCTAGCTATTTACTGTGAGAAGCGTTTTAAATACTCCGTTGACTTTGGACAG 306
Db	293	GAAAGATGTTCACAACTTATTACTGTCAAAAAGTATAACAGTGGCCCCACAGCGTTGGCCA 352
OY	307	GGTACCAAGGTGGAATAAAGCTACTGGCGGTGGTGGTTCTG 349
Db	353	GGGACCAAGGTGGAATAACGAAGCTGTGGCTGCACCATCTG 395

DEFINITION	60246328371 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576124 5', mRNA sequence.
ACCESSION	BG341941
VERSION	BG341941.1 GI:13148379
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 959)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: L1CML1288 row: e column: 21 High quality sequence step: 616.
FEATURES	Location/Qualifiers
SOURCE	1..959
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	/db_xref="taxon:9606"
	/clone="IMAGE:4576124"
	/clone_lib="NIH_MGC_48"
	/tissue_type="Primary B-cells from tonsils (cell line)"
	/lab_host="DH10B (phage-resistant)"
	/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."
BASE COUNT	244 a 265 c 232 g 218 t
ORIGIN	
Query Match	24.7%; Score 184.6; DB 152; Length 959;
Best Local Similarity	71.1%; Pred. No. 3.4e-46;
Matches	244; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
OY	7 GATATCCAGATGACCCAGTCCCGTCCTCCGTCGCGCTCTGTGGGCGATAGGCTACC 66
DB	54 GACATCCAGATGACCCAGTCCCGTCCTCCGTCGTCGATCTGTAGAGACAGAGCTACC 113
OY	67 ATCACCCTGGGGCGGCGACGCAAAACATCTATGGCGCGCGTGAATGATCAAGTAAACCT 126
DB	114 ATCACCCTGGCGGGCGAGTCAAGGCGATTAACAATTTTATAGCCTGTGATACGAGAACTA 173
OY	127 GCGAAGAGCTCCCAAGCTTCTGATTTACGCTGGAGCAACCTGGACAGATGAGATCCCTCT 186
DB	174 GGGAAAGTTCCCTAACACTCTGATCTATGCTGCATCCACTTTGCATTCACAGGGTCCCATCT 233
OY	187 GCGTCTCTGTGATCCGGCTCCGGAACGATTTCACTCTGACCATCAGCAGTCTGACGCT 246
DB	234 CGGTTCAAGTGGCAGTGGCTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGACGCT 293
OY	247 GAAGACTTCGCTAGCTATTCCTCAGAACGTTTAAATACCTCCGTTGCTTGGACAG 306
DB	294 GAAGATGTTTCAACTTATTAATCTCAAAAAGTATAACAGTGGCCCTCAGACGTTTGGCAA 353
OY	307 GGTACCAAGGTGAATAAAGCTACTGGCGGTGGGTGCTTG 349
DB	354 GGGACCAAGGTGAATAAAGCAACTGTGGCTGACCAATCTG 396

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RESULT 10
AW404714      608 bp      mRNA      EST      16-FEB-2000
LOCUS
DEFINITION   UI-HF-BL0-acd-c-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058580 5', mRNA sequence.
ACCESSION    AW404714
VERSION      AW404714.1 GI:6923771
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 608)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              cDNA Library Arrayed by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.

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      Location/Qualifiers
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        /db_xref="taxon:9606"
        /clone="IMAGE:3058580"
        /clone_lib="NIH_MGC_37"
        /tissue_type="lymph"
        /cell_type="germinal center B cells"
        /lab_host="MGC85"
        /note="Vector: p7T3-Pac; Site 1: NotI; Site 2: Eco RI;
              Constructed from size fractionated cytoplasmic mRNA
              (1.5-2.5kb). Directionally cloned. Cells provided by Louis
              M. Staudt, Ph.D. Library preparation by Maria de Fatima
              Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
  BASE COUNT  158 a 169 c 146 g 135 t
  ORIGIN
    10 ATCCAGATGACCCAGTCCCGTCCCTGTCGCGCTCTGTGGCGGATAGGCTCACCATC 69
    45 ATCCAGATGACCCAGTCCCATCTCCCTGTCGTGATCTGTAGGAGACAGATCACCATC 104
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    130 AAAGCTCGGAAGCTTCTGATTTACGGTGGGAGAACCTGGGAGGATGGATCCCTTCGCG 189
    165 AAAGCCCTTAACCTCTGATCTATGCTGCATCCAGTTTGAATAATGGGTCCTCATCAAG 224
    190 TTCTCTGATCCGCTCGGGAACGATTTCACTCTGACCATCAGCAGTCTGAGGCTGAA 249
    225 TTGAGTGCAGTGTGATCTGGGAGATTTCACTCTCAACATCAGGAGTCTGCAACCTGAA 284
    250 GACTTCGCTAGCTATTACTGTGACAGACGTTTAAATACTCTCCCTTTCGACAGAGGT 309
    285 GATTTCGAACCTACTCTGTGACAGAGATTTCACCTACCCCGTACAGTTTGGCCAGGG 344
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Db 345 ACAGACTGGAGATCAACGAAGTGTGGTGCACCATCTG 384

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RESULT 11
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LOCUS
DEFINITION   UI-HF-BL0-adg-h-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061499 5', mRNA sequence.
ACCESSION    AW406886
VERSION      AW406886.1 GI:6925943
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 431)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              cDNA Library Arrayed by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.

FEATURES
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      /tissue_type="lymph"
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      /lab_host="MGC85"
      /note="Vector: p7T3-Pac; Site 1: NotI; Site 2: Eco RI;
            Constructed from size fractionated cytoplasmic mRNA
            (1.5-2.5kb). Directionally cloned. Cells provided by Louis
            M. Staudt, Ph.D. Library preparation by Maria de Fatima
            Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
  BASE COUNT  101 a 125 c 105 g 100 t
  ORIGIN

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Query Match      24.5%; Score 183; DB 115; Length 431;
Best Local Similarity 70.8%; Pred. No. 8.5e-46;
Matches 243; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 7 GATATCAGATGACCCAGTCCCGTCCCTGTCGCGCTCTGTGGCGGATAGGTCACC 66
    11 1111111111111111111111111111111111111111111111111111111
Db 60 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCGTGATCTGTAGGAGACAGATCACC 119
    11 1111111111111111111111111111111111111111111111111111111
QY 67 ATCACCTCGGCGCCAGCAAAACATCTATGGCGGCTGAACCTGGATCAACGTAACCT 126
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Db 120 ATCACCTGGCGGCAAGTCAGACATTTAGCAGCTTTTAAATTTGATATCAGCAAAACCA 179
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QY 127 GGGAAAGCTCCGAAGCTTCTGATTTACGGTGGCAGCAACCTGGCAGATGAGTCCCTTCT 186
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QY 187 CGTTCTCTGATTCGGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGACGCT 246
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Db 240 AGTTTCAGTGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 299
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Db	438	ATCAAGGTTACGCGCAGTGGATATCGGACAGAAATTCACCTCTCAATCAACAGCCTGCA	379
Qy	243	GCCTGAAGACTTCGCTAGCTATTACTGTCGACAAAGCTTTTAATAATCTCGTTGACTTTTCGG	302
Db	378	GCCTGAAGATTTTGCACCTTATTACTGCTTCAGATAGTACTTACCCTTGGACTTTTGG	319
Qy	303	ACAGGGTACCAAGGTGGAATAAAACCTACTGCGGGTGGTGTCTG	349
Db	318	CCAGGGGACCAAGCTGGAGATCAAACGAACGTGGCTGCACCATCTG	272
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DEFINITION	602567476F1 NIH_MGC_77	Human sapiens cDNA clone IMAGE:4692138	5', mRNA sequence.
ACCESSION	BG539961		
VERSION	BG539961.1	GI:13532194	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1CM1512 row: g column: 19 High quality sequence stop: 704.		
FEATURES	Location/Qualifiers		
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	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1: SfiI (ggccattatggccc); Site:2: SfiI (ggccattatggccc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
BASE COUNT	241 a 250 c 217 g 159 t		
ORIGIN			
Query Match	24.3%	Score 181.6; DB 155; Length 867;	
Best Local Similarity	70.9%	pred. No. 2.8e-45;	
Matches	241; Conservative	0; Mismatches 99; Indels 0; Gaps 0;	
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Db	91	ATCCAGTTGACCCAGTCTCCCATCTCCCTGCTGTGCATCTGTAGGAGAGAGAGTACCATC	150
Qy	70	ACCTGGCGGCCGCGAAGAACATCTATGGCGCGCTGAACCTGGTATCAACGTAACCTGGG	129
Db	151	ACTTGCCGGGCAAGTCAGGCGATAGCAGTCTGTAGCCTGTATCAGCAAAAACCCAGG	210
Qy	130	AAAGCTCCGAAGCTTCTGATTTACGGTGCAGCAACCTCGCAGATGGAGTCCCTTCTCGC	189

[illegible]

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Db 181 ctttcgctctctctgattccggctccggaagcgatttcacacccatccagcagctc 240
OY 241 CAGCCTGAAGACTTCCTACGATTACTGTACAGAACGTTTTAAATACCTCGTACTTTC 300
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Db 241 cagcctgaagacttcctacgattactgtcagaagctttaaactccgtttgacttc 300
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OY 361 TCGGGTGGGGCGGTCTCTCAAGTCCAACTGATGTAATCCGGCGCGGAGTCAAGAGCA 420
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Db 421 ggggctcagtcgaaggtgtctgttaaagctagcggtatattttctaatltatgtgatt 480
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Db 601 tcgactagatacataataatgagctctccagctcgatcggagagcaagcgccgtcat 660
OY 661 TATTGCGCGCTTATTTTGTGTTCTAGCCCGAATTTGATTTGATTTGGGTTCAA 720
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Db 661 tattgcgcgcttattttgtgttctagccgaattgtattgtgttgggtcaaa 720
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Db 721 ggaacctgtctactgtctgacactga 747

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RESULT 3

AA08479
ID AA08479 standard; DNA: 747 BP.

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DE Murine 5G1.1M1 scFv DNA.
XX
XX Complement C5; haemolysis; kidney; glomerulonephritis;
KM monoclonal antibody; antinflammatory; antibody engineering;
KM humanised antibody; complementarity determining region; CDR;
KW scfv; single chain antibody; ds.
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XX 09-NOV-1995.
PD 01-MAY-1995; 95WO-US05688.
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PR 02-MAY-1994; 94US-0236208.
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XX (ALEX-) ALEXION PHARM INC.
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PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
XX
XX WPI: 1995-392923/50.
DR P-PSDB: AAR77606.
XX
XX Treating glomerulonephritis with antibody against complement C5
XX component - to inhibit complement induced cell lysis
XX
XX Claim 24; Page 107-110; 181pp; English.
XX
XX DNA (AA08479) coding for murine scFv 5G1.1M1 (AAR77606) was obt. by
XX PCR cloning of DNA from hybridoma ATCC HB 11625, the producer of
XX anti-C5 monoclonal antibody (Mab) 5G1.1. The DNA was subcloned into
XX pET Trc S05/Nr for expression in Escherichia coli. The light and/or
XX heavy chain CDRs of scFv 5G1.1M1 can be combined with CDRs from other
XX 5G1.1-derived antibodies, Fds and light chains (AAR77607-16) in the
XX prodn. of recombinant, including humanised, antibodies that retain
XX the ability of Mab 5G1.1 to block human complement C5a generation
XX and thus to reduce glomerular inflammation and kidney dysfunction
XX associated with glomerulonephritis.
XX
XX Sequence 747 BP; 183 A; 174 C; 211 G; 179 T; 0 other;
XX

```

Query Match 53.1%; Score 396.6; DB 16; Length 747;
Best Local Similarity 70.7%; Pred. No. 1.7e-101;
Matches 528; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

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OY 1 ATGGCGAATATCCATATGACCCAGTCCCGTCCCTGTCGCGCTGTGGGCAATAGG 60
    |||||||
Db 1 atggcgaaatattccatattgacccagttcccgctccctgtcgcgctgtgggcaatagg 60
OY 61 GTACACATCACCTGGCGGCCAGCAAAAACATCTATGCGCGCTGAACGTATACAGT 120
    |||||||
Db 61 gtacacatcacctggcgggccagcaaaaaacatctatgcgcgctgaacgtatcacagt 120
OY 121 AAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGGTGCAGCAACCTGGCAGTGAAGTC 180
    |||||||
Db 121 aaacctgggaaagctccgaagcttctgatttacgggtgcagcaacctggcagtgagtc 180
OY 181 CCTTCTCGTTCCTGAGATCCGCGTCCGAGACGATTTACCTGACATCGACGATCG 240
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Db 181 ccttctcgttctctgagatccgcgctccgagacgattttacctgacatcgcagtcgctg 240
OY 241 CAGCCTGAAGACTTCGCTACGATTACTGTACGAACGTTTTAAATACCTCGTACTTTC 300
    |||||||
Db 241 cagcctgaagacttcgctacgattactgtacgaacgTTTTAAATACCTCGTACTTTC 300
OY 301 GGACAGGGTACCAAGTGGAAATAAAACGTACTGCGGTGTCTGCTGGCGGTGGA 360
    |||||||
Db 301 ggacagggtaaccaaggtggaaaataaaaacgtactggcgggtgtctgctggcggtgga 360
OY 361 TCTGCTGTGCGGTCTCTCAAGTCCAACTGATGTAATCCGGCGCGGAGTCAAGAGCA 420
    |||||||
Db 361 tctgctgtgcggtctctcaagtccaaactgattgtaattccggcgcgaggtccaaaagcca 420
OY 421 GGGGCTCAGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTTATGAT 480
    |||||||
Db 421 ggggctcagtcgaaggtgtctgttaaagctagcggtatattttctaatltatgtgatt 480
OY 481 CAATGGGTGCTAGAGCCCGCGGAGGCGCTGGAATGATGGTGAGATCTTACCGGC 540
    |||||||
Db 481 caatgggtgctagagcccgcgagggcgctggaatgatggtgagatctttaccggc 540
OY 541 TCTGTAGCACCGAATATACGAAATTTTAAAGACCGTGTACTATGACGCGTGACACT 600
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Db 541 tctgtagcacccgaatataccgaaatTTTAAAGACCGTGTACTATGACGCGTGACACT 600

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Query Match	49.7%;	Score 371;	DB 16;	Length 750;
Best Local Similarity	97.4%;	Prod. No. 2.4e-94;		
Matches 377;	Conservative	0;	Mismatches 10;	Indels 0; Gaps 0;
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358	GGATCTGGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCCGAGGTCAAGAAG	417		
bb	37 gtaactgcggcgctcaactcccaagtcccaactggtgcaatccggcgcgaggtccaagaag	96		
418	CCAGGGCGCCTCAGTCAAAGTGCCTCTAAAGCTAGCGGCTATATTTTCTAATTATTGG	477		

478	ATTCAATGAGGTGGTTCAGGCCCGCCGAGCGCTGGAATGAGTGGGTGAGATCTTACCG	537
yy		
157	attcaatgggtcgctcagggccccggcgagcgctggaatgatgggtgagatcttaccg	216
bb		
538	GGCTCTGGTAGCACCGAATATACCGAAATTTTAAAGACCGGTCTTACTATGACGGCTGAC	597
yy		
217	ggctcggtagcaccgaaataacgaaaaattttaagacgggttactatgacgcggtgac	276
bb		
598	ACTTCGACTAGTACAGTATACATGAGAGCTCTCCAGCGCTCGCATCGGAGGACACGGCCGTC	657
yy		
277	acttcgactagtacagtatacacaTggagctctccagcctcgatccggagacacggccgctc	336
bb		
658	TATTANTGCCGGGTATTTTTTTGGTTCTAGCCCGAAATTGGTATTATTGATGTTTGGGCT	717
yy		

337 caccatttcgcgctcattatcttccagccccgaactcggcatcttgatgtttcggggc 396
 718 CAGGGAACCCCTGGTCACTGTCTCGAGC 744
 |||||
 b 397 caaggaaaccttggtcaactgtctcgagc 423
 RESULT 5
 AT08487
 D AAT08487 standard; DNA: 750 BP.

AAT08487;	
02-APR-1996	(first entry)
Humanised 5G1.1 VH + IGHRLD DNA.	
Complement C5; haemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR; ds.	
Synthetic.	
Key	Location/Qualifiers
CDS	1..750
	/*tag= a
sig_peptide	1..57
	/*tag= b
mat_peptide	58..747
	/*tag= c

[illegible]

ROCHER KP, SPRINGHORN J P, SQUINCO SF, THOMAS TC;
WANG Y, WILKINS JA;

Db 397 caagggaacctgtcactgtctcgagc 423
|||||

RESULT 7
AAT10706
ID AAT10706 standard; DNA; 726 BP.
XX AAT10706;
XX AC
XX 02-APR-1996 (first entry)
XX DE
XX Humanised 5G1.1 VL + KLV56B DNA.
XX KW
XX Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW ds.
XX Synthetic.

XX Key Location/Qualifiers
FH CDS 1..726
FT /*tag= a
FT sig_peptide
FT /*tag= b
FT mat_peptide 76..723
FT /*tag= c
XX WO9529697-A1.
XX 09-NOV-1995.
XX 01-MAY-1995; 95WO-US05688.
XX 02-MAY-1994; 94US-0236208.
XX (ALEX-) ALEXION PHARM INC.
XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
XX WPI; 1995-392923/50.
DR P-PSDB; AAR77613.
XX Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
XX Claim 42; Page 129-131; 181pp; English.

XX A DNA construct (AAT10706) codes for a humanised CDR-grafted and
CC framework sequence-altered light chain, 5G1.1 VL + KLV56B (AAR77613),
CC which includes CDRs derived from mouse anti-C5 monoclonal antibody
CC 5G1.1. The DNA can be subcloned together with DNA (AAT08483) coding
CC for a humanised Fd (AAR77610) into vector APEX-3P (AAT08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of MAb 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.

XX Sequence 726 BP; 175 A; 206 C; 187 G; 158 T; 0 other;

Query Match 44.0%; Score 328.8; DB 16; Length 726;
Best Local Similarity 96.6%; Pred. No. 1.5e-82;
Matches, 336; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 TGGCCGATATCCAGATGACCCAGTCCCGCTCTCCCTGTCCGCTCTGTGGCGGATAGGG 61
|||
Db 77 tgcaggtatccagatgacccagtcctccctgtccgctctgtggtcgataggg 136

QY 62 TCACCATCACCTGCGCGCCAGCGAAACATCTATGCGCGCTGAACCTGGTATCAACGTA 121
|||
Db 137 tcaccatcacctgctgctgagcgagcgaaacatctatgctgctgagcgatcaacgta 196
|||
QY 122 AACCTGGGAAGCTCCGAAGCTTCTGATTTACGTCGCGAAGACCTGGCAGATGGAGTCC 181
|||
Db 197 aacctgggaaagctccgaagcttctgatttacggtgcgaacacctggcagatcgagttcc 256
|||
QY 182 CTTCTCGCTTCTCTGGATCCGCTCCGGAACGGATTTCACCTGACCATCAGCAGTCTGC 241
|||
Db 257 cttctcgcttctctgctgctgctccggaacgatttcactctgaccatcagcagctgc 316
|||
QY 242 AGCTGGAAGACTTCGCTACGTATTACTGTCAGAACGTTTAAATACCTCGGTTGACTTTCG 301
|||
Db 317 agcctgaagacttcgctacgtattactgcagaacgcttttaatactcctgtgactttcg 376
|||
QY 302 GACAGGGTACCAGGTGGAAATAAAACGCTACTGCGCGTGGTGGTCTG 349
|||
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RESULT 8
AAT08486
ID AAT08486 standard; DNA; 711 BP.
XX AAT08486;
XX 15-MAR-1996 (first entry)
XX Humanised 5G1.1 VL + 012 DNA.
XX Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW ds.

XX Synthetic.

XX Key Location/Qualifiers
FH CDS 1..711
FT /*tag= a
FT sig_peptide 1..66
FT /*tag= b
FT mat_peptide 67..708
FT /*tag= c
XX WO9529697-A1.

XX 09-NOV-1995.
XX 01-MAY-1995; 95WO-US05688.
XX 02-MAY-1994; 94US-0236208.
XX (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
XX WPI; 1995-392923/50.

DR P-PSDB; AAR77614.

XX Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
XX Claim 35; Page 132-34; 181pp; English.

XX A DNA construct (AAT08486) codes for a humanised CDR-grafted
CC light chain, designated 5G1.1 VL + 012 (AAR77614), which includes
CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
CC DNA can be subcloned together with DNA (AAT08484) coding
CC for a humanised Fd (AAR77611) into vector APEX-3P (AAT08476) for

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Digan ME, Lake P, Wright RM;

DR WPI; 2000-482739/42.

DR P-PSDB; AAB07461.
XY

PT Recombinant immunotoxin used for prophylaxis and treatment of T-cell
PT mediated diseases e.g. transplantation rejection -

PS Disclosure; Page 55-59; 75pp; English

CC The present sequence encodes a recombinant immunotoxin comprising a
CC CD3-binding domain and a Pseudomonas exotoxin A component. It is
CC designated scFv(UCHL1)-PE28. The immunotoxins of the invention are
CC used for the prophylaxis or treatment of T-cell mediated diseases or
CC conditions of the immune system. They are also used to condition a
CC patient to be transplanted with cells, or a tissue or an organ of a
CC donor and for the prophylaxis and/or treatment of acute or chronic
CC transplantation rejection, host versus graft disease and/or graft
CC versus host disease in a patient to undergo a bone marrow transplant,
CC where the CD3-bearing cell population in the patient is depleted and
CC an inoculum comprising isolated bone marrow and/or stem-cell enriched
CC peripheral blood cells of the donor treated with immunotoxin is
CC inoculated into the patient.

50 Sequence 1803 BP; 363 A; 575 C; 567 G; 298 T; 0 other;

Query Match	36.18;	Score 269.4;	DB 21;	Length 1803;
-------------	--------	--------------	--------	--------------

Best Local Similarity 61.1%; Pred. NO. 86-66;
Matches 454: Conservative 0: Mismatches 2

machines 40%; conservative 0; mismatches 200; leaders 3; gaps 1;

QY	1	ATGGCCCATATCCGAGTACGACCAATCCCGCTCCCTGTCGCGGCTGTGGGGGGAATGG	60
Db	1	atggcgcgatattccgagtagcagaccgaatcccgctccctgtctcgtctctcgtcggagacaga	60
QY	61	GTCACCATCACTCTGGCGGCCGACGAGAAACATCTATGGCGCGCTGAACTGTATCAAGT	120
Db	61	gtcacccatcaactcttgccggcgccgacgagaaacatcttatggcgcgctgaaactgtatcaagt	120
QY	121	AAACCTGGGAAAGTCGCAAGCTTCTATTTACGGTGCAGCAACCGGGCAGATGGAGTC	180
Db	121	aaacctgggaaagtcgcgaagcttctatgtttacgggtgcagcaaacccgggacagatggagtc	180
QY	181	CGTTTCGCTTCTCTGGATCCGGCTCCGGAACGGATTTCATCTGACCATCAGACGTG	240
Db	181	ccatcaagttccagtcgtagcgagtcggtctcggaaacagattatctctccacatctagcaactg	240
QY	241	CAGCCTTAAGACTTCGCTACGATTAATTACTGTACAGACGTTTTAAATACTCCGTTCACTTC	300
Db	241	gagcaagagagatattgcacacttaactttgtccacaagaglaatacgtcttcgtagagctc	300
QY	301	GGACAGGGTACCAAGGTGGAAATTAACGATACATCTGCGCGTGTGGTTGGTGGC---	357
Db	301	gctgagagccacccaagctcggaaatcaacccgagctcggagcgagtagtcggtgagtcggt	360
QY	358	GGATCTGGTGGCGCGGTTTTCACAAAGTCAACTGGTGCATATCCGCGCGGAGGATCAAG	417
Db	361	ggagtcgagcgagtcggtgcgagatctgtagtcgagctcccaagagtcctggagcctcgtagaag	420
QY	418	CCAGGGGCGCTCAGTCAAAAGTGTCTCTGTAAAGCTTAGCGCGCTATATTTTCTTAATTATGG	477
Db	421	ccctgagcttcaatgaagaagataatactctgtagaagctctctgttatacattcattcgtctaac	480
QY	478	ATTTCATGGGTGCTCAGGCCGCCCGGCGAGGGCCTGGAATGATGGGTGAATCTTACCG	537
Db	481	attgacacgtgtgtagcgagagctatcgtgaagaacaccttgagtcgagtcacttaataacct	540
QY	538	GGCTCTGGTAGCACCGAATATACGGAATATTTTAAACACCGCTGTACTATAGACCGGTGAC	597
Db	541	taccacggctgttagtacctcaacccaagaattccaaggaacaggccaattaaactgtagac	600

OY 598 ACACGACTATTAAGATCATGTAGCTCCAGCCTGGAGTCGAGGACAGGCCGTC 657
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Db 601 aagcatccagcacgactacatgaacctccctcagtcgtcaacttgaagactctgcagtc 660
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Db 661 tattactgttgaaagatcggggtacttaacgftagatgtactgcattcgatctgtcgggc 720
CAAGGAACCTGTCACACTGCTC 740
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Db 721 gcagaggacaacagtcaaccgcttc 743

Search completed: July 20, 2001, 02:38:19
Job time: 4412 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 00:52:07 ; Search time 86.76 Seconds
(without alignments)
1629.961 Million cell updates/sec

Title: US-08-487-283A-8

Perfect score: 747

Sequence: 1 ATGGCCGATTCAGATGAC.....TGTCACCTCTCAGCTGA 747

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/1na/Backfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	294	39.4	819	2	US-08-400-115-3
2	283.4	37.9	723	1	US-07-988-430-92
3	283.4	37.9	723	1	US-08-425-336-89
4	283.4	37.9	723	1	US-08-488-113B-89
5	283.4	37.9	723	1	US-08-477-484B-89
6	283.4	37.9	723	2	US-08-646-360-89
7	283.4	37.9	723	3	US-08-839-765-89
8	283.4	37.9	723	3	US-09-136-389-89
9	283.4	37.9	723	5	PCT-US92-09487-92
10	267	35.7	1065	3	US-08-875-811-48
11	267	35.7	1074	3	US-08-875-811-44
12	267	35.7	1074	3	US-08-875-811-44
13	267	35.7	1074	3	US-08-875-811-50
14	267	35.7	1086	3	US-08-875-811-46
15	267	35.7	1137	3	US-08-875-811-42
16	250	33.5	729	1	US-08-230-843-3
17	250	33.5	729	2	US-08-636-936-3
18	247.2	33.1	916	1	US-08-121-054C-29
19	247.2	33.1	916	3	US-08-539-436-29
20	236.6	31.7	733	2	US-08-224-591-17
21	236.6	31.7	733	2	US-08-926-789-17
22	234.4	31.4	721	2	US-08-224-591-15
23	234.4	31.4	721	2	US-08-926-789-15
24	234.4	31.1	2178	1	US-08-463-587A-24
25	234.4	31.1	2178	2	US-08-463-587A-2
26	234.4	31.1	2178	2	US-08-923-854-24
27	234.4	31.1	2178	5	PCT-US91-09133-25

28	231	30.9	6727	2	US-08-125-462-2	Sequence 2, Appl
29	231	30.9	6727	2	US-08-891-848-2	Sequence 2, Appl
30	230.6	30.9	1299	2	US-08-125-462-6	Sequence 6, Appl
31	230.6	30.9	1299	2	US-08-891-848-6	Sequence 6, Appl
32	230.6	30.9	1320	2	US-08-125-462-3	Sequence 3, Appl
33	230.6	30.9	1320	2	US-08-891-848-3	Sequence 3, Appl
34	230.6	30.9	6799	2	US-08-125-462-5	Sequence 5, Appl
35	230.6	30.9	6799	2	US-08-891-848-5	Sequence 5, Appl
36	227.6	30.5	2143	3	US-09-097-309-5	Sequence 5, Appl
37	227.6	30.5	2143	4	US-09-097-111A-9	Sequence 9, Appl
38	227.6	30.5	6550	4	US-09-422-712B-1	Sequence 1, Appl
39	224.4	30.0	732	1	US-08-230-843-1	Sequence 1, Appl
40	224.4	30.0	732	2	US-08-636-936-1	Sequence 1, Appl
41	223.2	29.9	6127	2	US-08-887-352B-1	Sequence 1, Appl
42	223.2	29.9	6127	4	US-09-109-207C-1	Sequence 1, Appl
43	221.8	29.7	720	1	US-08-061-092A-2	Sequence 1, Appl
44	220.6	29.5	7305	1	US-08-286-740-4	Sequence 4, Appl
45	220.6	29.5	7305	5	PCT-US95-09576-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-400-115-3
; Sequence 3, Application US/08400115
; Patent No. 5864019
; GENERAL INFORMATION:
; APPLICANT: KING, David John
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; APPLICANT: YARRANTON, Geoffrey Thomas
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,115
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,136
; FILING DATE: 27-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,193
; FILING DATE: 17-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/00935
; FILING DATE: 11-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9012995.8
; FILING DATE: 11-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELETYPE: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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;      TOPOLOGY:  linear
;
;      FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..816
;
US-08-400-115-3

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Query Match	39.48;	Score 294;	DB 2;	Length 819;
Best Local Similarity	66.38;	Pred. No. 6.2e-84;		
Matches 439; Conservative	0;	Mismatches 220;	Indels 3;	Gaps 1

OY 4 GCGATATTCAGAAATGACCAGCTCCCGCTCCCTGCGCCCTGTGGCGAATTAAGGTC 63
 Db 64 GCTGATATTCAGAAATGACTGCTCCAGCTCCCTATCTGTATCTGGGAGAACTGTC 123
 OY 64 ACATATCACCTCGCGCGCCAGCAAAACATCTATGGCGCGCTGAACGTGTACAGTA 123
 Db 124 ACATATCACATGTGCGAAGCAACTGAGAAATATTTACAGTAATTTAGCATGTATCAACAGAAA 183
 OY 124 CTTGGGAAAGCTCCGAAGCTTTCTGATTTACGGTGCAGCAAGCACTGGCAGATGGAGTCCT 183
 Db 184 CAGGAAAAATCTCCTCAGCTCTGCTGTCTATGTGCAACAAATTTAGAGATGGTGTGCCA 243
 OY 184 TCTGTCTTCTCTGATCTCCGCTCCGGAACGATTTCTACTGTGACATCAGCACTGTGCAG 243
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 Db 304 TCTAAGAAATTTTGGAGTTATTTACTGTCAACATTTTGGGGTACTCCTGACAGCTTGCGA 363
 OY 304 CAGGATCCAAAGGTGAAATPAAACGATCTACGCGGTGTGTTCTGTGCGCGGTGATCT 363
 Db 364 GGGGGGACCAAGCTTGAATATAAACG---TGTGGCGGGGAGATCCGGCGGGGAGTTCA 420
 OY 364 GGTGTGTGGCGGTTCTCAAGTCCAACTGTGTSCAAATCCGGCGCGGAGGTCAAGAACGAGG 423
 Db 421 GGGGTGTGGCGGATCCAGGTTCAGCTCAGCAAGTCTGACCTGTAGTGTGGAACTCGGG 480
 OY 424 GCTTCATCAAAAGTCTCTGTAAGAGCTAGCGGCTATATTTTTCATAATTTTGATTTCAA 483
 Db 481 GCTTCATGGAAGATATCTCTCAAGGCTTCGCTACCTTCACCTGACATGCTATTCAC 540
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 OY 604 ACTATGACAGTATACATGAGAGCTCTCCAGCCTGCGATCGGAGGACAGCGCGCTATAT 663
 Db 661 TCCAGCACTGCTATCAGTACAGGCTCAACAGCCTGACATCTGAGATTTCTGAGATGTATTC 720
 OY 664 TG 665
 Db 721 TG 722

RESULT 2
 US-07-988-430-92
 : Sequence 92, Application US/07988430
 : Patent No. 5416202
 GENERAL INFORMATION:
 : APPLICANT: Bernhard, Susan L.
 : APPLICANT: Better, Marc D.
 : APPLICANT: Carroll, Stephen F.
 : APPLICANT: Lane, Julie A.
 : APPLICANT: Lei, Shau-Ping
 : TITLE OF INVENTION: Materials Comprising and Methods of
 : Preparation and Use for Ribosome-Inactivating Proteins
 : NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 541620and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ. ID. NO.: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

Query Match	37.9%	Score 283.4	DB 1	Length 723
Best Local Similarity	63.7%	Pred. 0.1, 4e-80		
Matches	472	Conservative	0	Mismatches 251; Indels 18; Gaps 2;
QY	7	GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCCCTCTGTGGCGGATAGGTCACC	66	
DB	1	GACATCCAGATGACATCAGTCCATCTTCCCTGCTGCATCTGTAGAGACAGAGTACT	60	
QY	67	ATCACCTGCGGGGCCAGCGAAACATCTATGGCGGGCTGAACTGGTATCAAGTAAACT	126	
DB	61	ATCACCTTCCCGGGGCGAGTCAGCAGCATTTATATACCTTTTAAAGTGGTTCAGAGAAACCA	120	
QY	127	GGGAAGGCTCCGAACCTTCTGATTTACGGTGGGAGCAACTGGAGATGAGTCCCTTCT	186	
DB	121	GGGAAGGCTCCATMAACCCCTGATCTATGCTGCAACACAGTTGGATCTGGGTTCCCATCA	180	
QY	187	GCCTTCTCTGGATCCGGCTCCGGAAAGGATTTCACTCTGACCATGACATGTGCAGCCT	246	
DB	181	AGGTTCAAGTGCAGTAGGATCTGGGACAGATTTACTCTCCACCATGACGAGCCTCGAATAT	240	
QY	247	GAAGACTTCGCTAGCTATTACTGCTAGAAACGTTTAAATACCTCGGTGACTTCCGACAG	306	
DB	241	GAGAGTTTGTGAATTTATTTATGTACACGATGATGATGATCTCCGCTGGACGTTCCGTGCA	300	
QY	307	GGTCAAGAGGTGGAATATAACGTACTGGCGGTGTGTGTTCTGTGGCGGTGATCTGGT	366	
DB	301	GGCACCAAGCTTGAAGATGAAA-----GGTGGCGGTGGATCTGGTGGAGGTGGTCCGGA	354	
QY	367	GGTGGCGGTTCCTCAAGTCCCACTGGTGCATCCGGCGCCGAGGTCAAGAAGCAGAGGGCC	426	
DB	355	GGTGGAGGATGTGAATCCAGTTGGTGTGAGTCTGGAGGAGGCGCTGTGAAGCCTTGAGAGG	414	

427 TCAGTCAAGTCTCCTGTAAACCTACCGCTATATTTTCTATATTGATTCATG 486
415 TCCGTCAAGATCTCTCCGACCTCTCTGCTATACCTTACAACTATGAATGACTGG 474
487 GTGCGTCAAGGCCCCGCGAGGCTGGAATGATGGAGATCTTACCGGCTCTGCT 546
475 GTGCGCCAGGCTCCAGGAAGGTTAGATGATGGCTGGATTAACACCCACACTGGA 534
547 AGACCGAATATACGGAATTTTAAAGACCGTTACTATGACCGGTACACTTGACT 606
535 GAGCAACATATGATGATCTTTCAAGGAGGTTACTCTCTTGGACGATTTCTAAG 594
607 AGTACAGTATACATGAGCTCTCCAGCTGCGATGCGAGACAGCGCCGTATATTCG 666
595 AACACTGCTATTTACAGATCAACAGCCTCAGAGCCGAGACAGCGCTGTATTTCTGT 654
667 GCGGCTATTTTGTGTTCTAGCCGAAATTTGATTTGGGTCAGGAAC 726
655 ACAGACGCGGTTACG-----ACTGTACTTCTGATGTCTGGGCGCAAGGAGCC 702
727 CTGCTCACTGTCTCGAGCTGA 747
703 ACGTCAACGCTCTCCATGA 723

RESULT 3
US-08-425-336-89
Sequence 89, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-425-336-89

Query Match 37.9%; Score 283.4; DB 1; Length 723;
Best Local Similarity 63.7%; Pred. No. 1,4e-80;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

7 GATATCCAGATGACCCAGTCCGCTCCCTGCTGCGGCTGTGGGGGATAGAGTACC 66
1 GACATCCAGATGACCTCAGTCTCCATCTTCCCTGCTGCTGATGTAGGAGACAGTCACT 60
67 ATCACTGCGCGCGCAGGAAACATATGAGCGCGCTGAACCTGATCAACGTAACCT 126
61 ATCACTTCCGCGCGGAGTACAGACATTAATGATTAATTAAGCTGGTTCCACAGAACCA 120
127 GGGAAAGCTCCGAAGCTTCTATTTACGCTCGAGAACCTGGCAGATGAGTCCCTTCT 186
121 GGGAAAGCTCTTAAGACCCCTGATATCTGCAAAACAGATTGGATCTGGGCTCCATCA 180
187 CGCTTCTGTGATCCGCGTCCGGAACGATTTCACTCTGACATCAGCAGCTGAGCT 246
181 AGTTCACTGAGTGGAGTGTCTGGACACAGATTAATCTCACACATCAGCAGCTGCAATAT 240
247 GAAGACTTCCGCTACGATATTAATCTGAGAACGTTTAAATACCTCGTTGACTTTGAGACG 306
241 GAAGATTTTGGAAATTTATTTATGTCACACAGATGATGATGATGATGATGATGATGATG 300
307 GGTACCAAGGTGGAATTAACGATCTGCGGCTGCTGTTGTTGCTGCTGCTGCTGCTGCT 366
301 GGCACCAAGCTTGAATGAATAA-----GGTCCGCTGATCTGCTGCTGCTGCTGCTGCTGCT 354
367 GGTGCGGCTTCTCAAGTCCAACTGCTGATCCGCGCGCGCGGAGTCAACAGCCAGGCGC 426
355 GGTGAGGATCTGAGATTCAGTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 414
427 TCAGTCAAGTGTCTCTGTAAGCTAGCGGCTATATTTTCTTAAATATTTGATTCATG 486
415 TCCGTCAAGATCTCTCTGCGCAGCTTCTGCTGATACCTTCAAACTATGATGATGATG 474
487 GTGCGTCAAGGCCCCGCGAGGCGCTGGAATGATGAGTGTGATCTTACCGGCTCTGCT 546
475 GTGCGCAGGCTCCAGGAAGGTTAGATGATGAGTGTGATGATGATGATGATGATGATG 534
547 AGCAGCAATATACGGAATTTTAAAGACCGTGTACTATAGCCGCGACACTTCGACT 606
535 GAGCAACATATAGCTGATCTTTCAAGGAGGTTTACCTTCTTGGACGATTTCTAAG 594
607 AGTACAGTATACATGAGCTCTCAGCCTGCGATCGAGACAGCGCGCTATATTATTCG 666
595 AACACTGCTATTTACAGATCAACAGCTCAGAGCGAGGACAGCGCTGTATATTCTGT 654
667 GCGGCTATTTTGTGTTCTAGCCGAAATTTGATTTGATTTGGTGGGCTCAAGAAC 726
655 ACAAGACGCGGTTACG-----ACTGTACTTCTGATGTCTGGGCGCAAGGAGCC 702
727 CTGCTCACTGTCTCGAGCTGA 747
703 ACGTCAACGCTCTCCATGA 723

RESULT 4
US-08-488-113B-89
Sequence 89, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins

```

NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70..P3..C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-113B-89

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Query Match      37.9%; Score 283.4; DB 1; Length 723;
Best Local Similarity 63.7%; Pred. No. 1.4e-80;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

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QY 307 GGTACCAAGGTGGAATAAAGCTACTGCGCGTGTCTGCTGCGCGGTGATCTGCT 366
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DB 301 GGCACCAACCTTGAGATGAAA-----GGTGGCGGTGAGATCTGTGAGGTGCGGGA 354
QY 367 GGTGGCGGTTCACAGTCAACTGCTGCAATCCGGCGCCGAGGTCAAGAACCGAGGGCC 426
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 355 GGTGGAGATCTGAGATCCAGTTGGTCAGTCTGGAGAGGCCCTGGTGAACCTGGAGGG 414
QY 427 TCAGTCAAGTGTCCCTGAAGCTACCGGCTATATTTTCTATATATGATTCATG 486
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 415 TCCGTGAGATCTCTCGCGACCTCTGCTGATACCTTACAACTATGAAATGAAGCTG 474
QY 487 GTGCGTACGCCCCCGGAGGCGCTGGAATGAGTGGTGAATCTTACCGGGCTGTG 546
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 GTGCGCGAGGCTCCAGAAAGGTTTGAATGATGGCTGGATTAACACCCACATGGA 534
QY 547 AGCACCGAATATACGAAATTTTAAAGACCGTGTACTATGACGGGTGACACTTGC 606
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 535 GAGCCAAATATGCTGATCTTCTTCAAGGAGCGGTTTAACTTCTTGGACATCTAAG 594
QY 607 ACTACAGTATACATGAGCTCTCCACCTCGATCGGAGACACGGCCGTCTATTTGC 666
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 595 AACACTGCTATTTACAGATCAACACCGCTCAGAGCCGAGACACGGCTGTATTTCTGT 654
QY 667 GCGCGTATTTTGTGTTCTAGCCGGAATGATTTGATTTGTTGGGCTCAAGAAC 726
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 655 ACAAGACGGGGTTAGC-----ACTGTACTTGCATGTCTGGGCGCAAGGGACC 702
QY 727 CTGCTCACTGTCTCGAGCTGA 747
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DB 703 ACGGTACCGCTTCCCTCATGA 723

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RESULT 5
US-08-477-484B-89
; Sequence 89, Application US/08477484B
; Patent No. 5756699
;
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studilka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 89:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-477-484B-89

Query Match 37.9%; Score 283.4; DB 1; Length 723;
 Best Local Similarity 63.7%; Pred. No. 1.4e-80;

Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

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QY 7 GATATCCAGATACCCAGTCCCGTCCCTGTCGCGCTCTGTGGCGATAGGTCACC 66
Db 1 GACATCCAGATACCTACGATCTCCATCTCCCTGTGATCTAGACAGACAGTCACT 60
QY 67 ATCACTGGGGGGCCGCAAAACATCTATGGCGCGCTGACATCGATCAACGTAACCT 126
Db 61 ATCACTGGCGGGCGAGTGAAGGACATTAATAGCTATTAAGCTGGTCCAGCAAGAACCA 120
QY 127 GGAAGAAGCTCCAGAGTCTGTATTTACGGTGCAGCAGACCTGCGAGATGAGTCCCTCT 186
Db 121 GGAAGAAGCTCCAGAGTCTGTATTTACGGTGCAGCAGACCTGCGAGATGAGTCCCTCT 180
QY 187 CGCTTCTCTGGATCCGGCTCCGAGACGATTCACCTCTGACATCAGACGATCTGCAGCT 246
Db 181 AGCTTCAGAGGAGTGGATCTGGGACAGATTAATACCTCACCATCAGCAGCTGCATAT 240
QY 247 GAAGACTCGCTACGATTAAGTCTCAGACGTTTAAATACCTCCGTTGATTCGGGACAG 306
Db 241 GAAGATTTTGAATTTATTTATTTGTCACAGTATGATGAGTCTCCGTTGAGCTTGGTGA 300
QY 307 GGTACCAAGTGGAAATAAAGCTACTGCGGCTGTGTCTGTGGCGGTGATCTGCT 366
Db 301 GGCACCAAGCTTGATGAAA-----GGTGGCGGTGATCTGTGGAGGTGGTCCGGA 354
QY 367 GGTGGCGGTCTCAAGTCAAGTGTGCAATCCGGCGCGAGGTCAAGAACCCAGGGGCC 426
Db 365 GGTGGAGGATCTGAGATTCAGTTGGTGGTGCAGTCTGAGAGGCGCTGGTGAAGCCCTGGAGG 414
QY 427 TCAGTCAAAAGTCTCTGTAAGCTTACGGCTATATTTTCTTAATATTGATTCATG 486
Db 415 TCCGTCAGATATCTCCGCTGCTCTGCTGATACCAATATGAAATGAATGG 474
QY 487 GTGGCTCAGGGCCCGGGGAGGGGCTGGAATGGATGGATGATCTTACGGGCTCTGCT 546
Db 475 GTGGCCGAGGCTCCAGGAAGGGTTTGAATGATGGCTGATTAACACCCACACTGGA 534
QY 547 AGCACCAGATATACGAAATTTTAAAGACGCTTACTATGACGCGTACACTTGCAGCT 606
Db 535 GAGCCACATATATGATCTCTTCAAGGACGCTTACCTCTCTTTGGACGATCTCAAG 594
QY 607 AGTACAGTATACATGAGAGCTTCACAGCTGCATGCGAGACACAGCGCGCTATTTATTC 666
Db 595 AACACTGCTATTTACATGATCAACAGCTCAGAGCCGAGACACGCGCTGTGATTTCTGT 654
QY 667 GCGGCTATTTTGGTCTAGCCCGAATTTGATTTTGTGATTTTGGGCTCAAGAAC 726
Db 655 ACAGACAGGGGTTAGC-----ACTGTACTTGATGTCTGGGGGCAAGGACC 702

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QY 727 CTGGTCACTGTCTGAGCTGA 747
 Db 703 ACGTCAAGCTCTCTCATGA 723

RESULT 6
 US-08-646-360-89
 Sequence 89, Application US/08646360
 Patent No. 5837491
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 89:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-646-360-89

Query Match 37.9%; Score 283.4; DB 2; Length 723;
 Best Local Similarity 63.7%; Pred. No. 1.4e-80;
 Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

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QY 7 GATATCCAGATACCCAGTCCCGTCCCTGTCGCGCTCTGTGGCGATAGGTCACC 66
Db 1 GACATCCAGATACCTACGATCTCCATCTCCCTGTGATCTAGACAGACAGTCACT 60

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OY 67 ATCACCCTGGGGGCGGAGGAGGAAACATCTATGCGCGCTGAACCTGATCAACGTAACCT 126
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Db 61 ATCACTTGGCCGGGAGAGTCAGACATTAATAGCTATTAAGCTGTCCAGAGAAACA 120
OY 127 GGGAAAGCTCCGAAGCTTCTATTTACGGTCGACGAACCTGGCAGATGAGCTCCCTCT 186
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Db 121 GGGAAACCTCCAGAACCTGATCTATGTCGCAACACATGGAATCTGGGGTCCCATCA 180
OY 187 CGCTCTCTGATCGGCTCGGAGACGATTTCACTGACCATCAGACGCTGAGGCT 246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AGCTTCAGTGGCAGATGATCTGGGACATTAATCTCACCATCAGACGCTGCAATAT 240
OY 247 GAAGACTTCCGCTAGTATTAATCTGCAAGCGTTTAAATCTCCGTTACTTTCCGACAG 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAAGATTTTGAATTTATTTATTTGCAACAGATATGATGATCTCCGTCGACGTTGGTGA 300
OY 307 GGTACCAAGGTGGAATTAACCTGACTGCGGTGCTGTTGTTGGTGGGCTGATCTGCT 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GGCACCAAGCTTGAGATGAAA-----GGTGGCGGTGATCTGCTGGAGTGGGTCCGGA 354
OY 367 GGTGGCGGTCTCAAGTCCCACTGGTCAATCCGGCGCGGAGCAAGCCAGGGGGCC 426
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Db 355 GGTGGAGGATCTGAGATTCAGTGTGTCAGTCTGAGAGAGGCTGTTGAGGCTGGAGGG 414
OY 427 TCAGTCAAGGTCTCTGTAAAGCTAGCGCTATATTTTCTAATTATTTGATTCATGCG 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 TCCGTCAAGATCTCCTGGCGAGGCTCTGGGTATACCTTCACAACTATGGAATGAATGG 474
OY 487 GTGGGTACAGGCCCCCGGAGGCTGGAATGATGGTGAATCTTACCGGGCTCTGCT 546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 GTGGCGCAGGCTCCAGGAAAGGTTTAAAGTGATGGCTGATTAACCCACCACTGTA 534
OY 547 AGCACCGAATTAACGAAATTTTAAAGACCGTCTTACTATGACGCGTACACTGCACT 606
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 GAGCCACATATGCTGATCTTTCAAGGAGCGGTTTACCTCTCTTTGACCATTTCTAG 594
OY 607 AGTACAGTATACATGAGACCTCTCCAGCTGATGAGAGACACCGCGCTATTATTGTC 666
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 AACACTGGCTATTACATCAACAGCCTCAGAGCCGAGAGCGCTGTATTTCTGT 654
OY 667 GCGGCTATTTTGTGTTCTAGCCCGCAATTTGATTTGATTTGGGTGTAAGAACCT 726
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 ACAAGAGCGGGGTTAGC-----ACTGTACTTCTGATCTGGGGCCCAAGGAGCC 702
OY 727 CTGCTCACTGTCTCGAGCTGA 747
    ||||| ||||| ||||| |||||
Db 703 ACGGTCAACCTCTCTCATGA 723

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APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEO ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-839-765-89

Query Match      37.9%; Score 283.4; DB 3; Length 723;
Best Local Similarity 63.7%; Pred. No. 1.4e-80;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

```

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OY 7 GATATCCAGATGACCCAGTCCCGCTCTCCGCTCTGTGGGCAATGAGGTACCC 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GACATCCAGATGACCTGACCTCCATCTTCCATCTGCTGCACTGTAGAGACAGATCACT 60
OY 67 ATCACCCTGGGGGCGGAGGAGGAAACATCTATGCGCGCTGATGAGTCCGTAACGTAACCT 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ATCACTTGGCCGGGAGAGTCAGACATTAATAGCTATTTAAGCTGTCCAGAGAAACA 120
OY 127 GGGAAAGCTCCGAAGCTTCTGATTTACGTCGACGAAACCTGGCAGATGAGCTCCCTCT 186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GGGAAAGCTCCGAAGCTTCTGATTTACGTCGACGAAACCTGGCAGATGAGCTCCCTCT 180
OY 187 CGCTCTCTGATGATCGGCTCCGAGACGATTTCACTCTGACATCAGACAGTCTGACCT 246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AGCTTCAGTGGCAGTGTGATCTGGGACAGATTAATCTCACCATCAGACCTGCAATAT 240
OY 247 GAAGACTTCCGCTAGTATTAATCTGCAAGACGTTTAAATCTCCGTTACTTTCCGACAG 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAAGATTTTGAATTTATTTATTTGCAACAGATATGATGATGCTGAGAGTTCGGGGA 300
OY 307 GGTACCAAGGTGGAATTAACCTGACTGCGGTGATGATGATGATGATGATGATGATGAT 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GGCACCAAGCTTGAGATGAAA-----GGTGGCGGTGATCTGCTGGAGTGGGTCCGGA 354
OY 367 GGTGGCGGTCTCAAGTCCCACTGTCGAATCCGGCGCGGAGGTCAAGAACGAGGGGCC 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 GGTGGAGGATCTGAGATCCAGTGTGTCAGTCTGAGAGAGGCTGGGAGGCTGGAGGG 414
OY 427 TCAGTCAAGGTCTCTGTAAAGCTAGCGCTATATTTTCTAATTATTTGATTCATGAG 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 TCCGTCAAGATCTCCTGGCGAGGCTTCTGGGTATACCTTCAACACTATGGAATGAATGG 474
OY 487 GTGGGTACAGGCCCCCGGAGGCTGGAATGATGGTGAATGATGATGATGATGATGATGAT 546

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Db 475 GTGGCGCAGGCTCCAGGAAGGTTAGATGGATGGCTGATTAACACCCACACTGGA 534
Oy 547 AGCACCAGATATACGAAATTTTAAAGACCGTGTATGACGCGTACACTTGCAGT 606
Db 535 GAGCCAAATATGCTATCTTCAAGGACGCTTACCTTCTTGTGACGATTTCAAG 594
Oy 607 AATACAGTATACATGAGCTCTCCAGCTCCGATCGAGAGACAGCGCGTCTATTATGC 666
Db 595 AACACGCTATTTTACAGATCAACAGCTCAGAGCGAGAGACGCGTGTATTCTGT 654
Oy 667 GCGCGTATTTTGTGTTCTACCGCAATTTGATTTGATTTGGGTCAGGAAGACC 726
Db 655 ACAAGACGGGTTAGC-----ACTGTTACTTGCATGTCTGGGCCAAGGACCC 702
Oy 727 CTGGTACTGTCTGAGCTGA 747
Db 703 ACGTCAACGCTCCTCATGA 723

RESULT 8
US-09-136-389-89
; Sequence 89, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studlika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESS: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70, P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 89:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-136-389-89

Query Match 37.9%; Score 283.4; DB 3; Length 723;
Best Local Similarity 63.7%; Pred. No. 1.4e-80;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

Oy 7 CATATCCAGATGATCCCATCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 66
Db 1 GACATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
Oy 67 ATACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 126
Db 61 ATACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Oy 127 GGAAGAGCTCCGAAAGCTTCTGATTTACGTTGCGGAGCAAGCTGCGAGATGAGTCCCTTCT 186
Db 121 GGAAGAGCTCCGAAAGCTTCTGATTTACGTTGCGGAGCAAGCTGCGAGATGAGTCCCAATCA 180
Oy 187 CGCTTCTCTGATCCGCTCCGGAACGATTTCACTCTGACCATGACAGTCTGACGCT 246
Db 181 AGCTTCACTGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 240
Oy 247 GAAGCTTCGCTACTATTTACGTTGAGAAAGCTTTAAATACGCTGCTTGTGAGAG 306
Db 241 GAAGATTTTGGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 300
Oy 307 GTATCAAGAGTGAATTAAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 366
Db 301 GGCACCAAGCTTGAATGAATA-----GGTGGCGGTGATCTGTGTGTGTGTGTGTGTGTGT 354
Oy 367 GGTGGCGGTGCTCAAGTCCAGTGTGCAATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 426
Db 355 GGTGGAGATGCTGAGATCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 414
Oy 427 TCAATCAAGTGTCTCTGTAAGCTGAGCGCTATTTATTTTCTAATTTATTTGATTTCAATGG 486
Db 415 TCCGTCAGAAATCTCTGCGGCACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 474
Oy 487 GTGGTCAAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 546
Db 475 GTGGCGCAGGCTCCAGGAAGGTTAGATGGATGGCTGATTAACACCCACACTGGA 534
Oy 547 AGCACCAGATATACGAAATTTTAAAGACCGTGTACTATGACCGTGTACACTTGCAGT 606
Db 535 GAGCCAAATATGCTATCTTCAAGGACGCTTACCTTCTTGTGACGATTTCAAG 594
Oy 607 AATACAGTATACATGAGCTCTCCAGCTCCGATCGAGAGACAGCGCGCTATTATTTGC 666
Db 595 AACACGCTATTTTACAGATCAACAGCTCAGAGCGAGAGACAGCGCTGTATTCTGT 654
Oy 667 GCGCGTATTTTGTGTTCTAGCCGAATTTGATTTTGAATTTGGGTCAGGAAGACC 726
Db 655 ACAAGACGGGTTAGC-----ACTGTTACTTGCATGTCTGGGCCAAGGACCC 702
Oy 727 CTGGTACTGTCTGAGCTGA 747
Db 703 ACGTCAACGCTCCTCATGA 723

RESULT 9
PCT-US92-09487-92
; Sequence 92, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

```



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: LENGTH: 1065 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1065
: OTHER INFORMATION: /note="sfvbmctluonc"
:
: US-08-875-811-40

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Query Match          35.7%; Score 267; DB 3: Length 1065;
Best Local Similarity 63.4%; Pred. No. 2.7e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

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Oy 7 GATATCCAGATGACCCAGTCCCGCTCCCTCTGCGGCGGAGTGGAGTACC 66
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Db 1 GACATCAATGACCCAGTCTCATCTTCATGTATGATCTAGAGAGAGTCACT 60

Oy 67 ATACCTGGGCGCCAGCAAAACATCTATGCGCGCTGAACGTGATCAACGTAACT 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TTCACTTGCAGGCGAGTGAAGCAATTAATTAATTAATTAATTAATTAATTAATTA 120

Oy 127 GGGAAAGCTCCGAGCTTGTGATTTACGGTGCAGCAACCTGGCAGATGAGTCCCTTCT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GGGAAATCTCTAAAGCCCTGATCTATCGTCAAAACGAGCTGGATGGGCTCCATCA 180

Oy 187 CGCTTCTGATCCGCGTCCGAGAGGATTTCACTGTACCATTCACAGCTCCAGCT 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AGTTTAGTGGAGTGGATGTGACAAAGATTATTTCTCACCTTACAGCTGAGATAT 240

Oy 247 GAAGACTTGGCTACGTATCTGTAGAACGTTTAAATACCTGTTGACTTTCGACAG 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GAAGATATGGAAATTAATTAATGTCTACAGTATGATGATGATGATGATGATGATG 300

Oy 307 GGTACCAAGTGGAAATAAAGCTACTGGCGGTGGTGTCTGTGCGGCTGATCTGCT 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GGGACCAAGCTGGAAATAA-----GGAGCGGTGGTCTGGCGGATCGGGT 354

Oy 367 GGTGGCGGTTCTCAATGCCAAGTGTGCATTCGGCGCGGAGGTCAGAAAGCCAGGGGCC 426
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 GCGGCGGCTCTGAGTTTCACTTCAGCTCCAGCACTGTGGACTTACTGGCAAGCGCTGGGGCT 414

Oy 427 TCAGTCAAAAGTCTCTGTAAAGCTAGCGGCTATATTTTCTAATTAATGATCAATGG 486
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 415 TCAGTCAAAAGTCTCTGTAAAGCTAGCGGCTATATTTTCTAATTAATGATCAATGG 474

Oy 487 GTGCGTCAAGCGCGCGGCGAGGCGCTGGAAATGATGGGTAGATCTTAACGGGCTGTGCT 546
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Db 475 ATAAACACAGAGGCTGGACAGGCTGTGACTGCTGCTATTTGATCTCGAAATAGT 534

Oy 547 AGCAGCGAATATACGAATTTTAAAGCCGTGTTACTATGACGGCTGACACTTCCACT 606
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 GATTAATTTTACACCGCAATTCACACACAGAGCCAAAGCTGAGTACTCCACCC 594

Oy 607 AGTACAGTATACATGAGGCTCTCCAGCTGCGATCGGAGACAGCGCGCTTATTAATGG 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 AGCAGTCTAGTACGATGACCTCAACAGCGCTGACAAATGAGAGCTGTGGGTCTATTACTGT 654

Oy 667 GCGCGTATATTTT 679
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Db 655 ACCCGCTTTAT 667
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RESULT 11
US-08-875-811-48
: Sequence 48, Application US/08875811
: Patent No. 6045793
:
: GENERAL INFORMATION:
: APPLICANT: Rybak, Susanna M.
: APPLICANT: Newton, Dianne L.
: APPLICANT: Boque, Luis

```

```

: APPLICANT: Wlodawer, Alexander
: TITLE OF INVENTION: Recombinant Ribonuclease Proteins
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/875,811
: FILING DATE: 19-FEB-1998
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US97/02588
: FILING DATE: 19-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/011,800
: FILING DATE: 21-FEB-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Faris, Susan K.
: REGISTRATION NUMBER: 41,739
: REFERENCE/DOCKET NUMBER: 015280-244100US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
:
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1065 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1065
: OTHER INFORMATION: /note="sfvbmctluonc"
:
: US-08-875-811-48

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Query Match          35.7%; Score 267; DB 3: Length 1065;
Best Local Similarity 63.4%; Pred. No. 2.7e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

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Oy 7 GATATCCAGATGACCCAGTCCCGCTCCCTCTGCGGCGGAGTGGAGTACC 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GACATCAATGACCCAGTCTCATCTTCATGTATGATCTAGAGAGAGTCACT 60

Oy 67 ATACCTGGGCGCCAGCAAAACATCTATGCGCGCTGAACGTGATCAACGTAACT 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TTCACTTGCAGGCGAGTGAAGCAATTAATTAATTAATTAATTAATTAATTAATTA 120

Oy 127 GGGAAAGCTCCGAGCTTGTGATTTACGGTGCAGCAACCTGGCAGATGAGTCCCTTCT 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GGGAAATCTCTAAAGCCCTGATCTATCGTCAAAACGAGCTGGATGGGCTCCATCA 180

Oy 187 CGCTTCTGATCCGCGTCCGAGAGGATTTCACTGTGACCATGACAGTCTGAGCT 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AGTTTAGTGGAGTGGATGTGACAAAGATTATTTCTTCACATTAAGCAGCTGAGATAT 240

Oy 247 GAAGACTTGGCTACGTATTAATGATGAGAACGTTTAAATACTCCGTTGACTTTCGAGAC 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GAAGATATGGAAATTAATTAATGTCTACAGTATGATGATTTCCGATACGTTCCGAGGG 300

Oy 307 GGTACCAAGTGGAAATAAAGCTACTGGCGGTGGTGTGCTGTGCGGCTGATCTGCT 366
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Db 301 GGGACCAAGCTGGAAATAA-----GGAGCGGTGGTCTGGCGGATCGGGT 354

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Query Match 35.7%; Score 267; DB 3; Length 1086;
Best Local Similarity 63.4%; Pred. No. 2.7e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCATCCCGCTCTCCCTGTCGCGCTGTGGCGATAGGGTACC 66
DB 361 GACATCAAGATGACCCATCCCGCTCTCCCTGTCGCGCTGTGGCGATAGGGTACC 420
QY 67 ATCACTGCGCGCGACGAGGAAACATCTATGCGCGCTGTAAGTATCAAGTAACT 126
DB 421 TTCCTTGCAAGGAGGAGTCAGACATTAATACTATTATGCTGCTCCAGAGAAACA 480
QY 127 GGAAGAGCTCCGAACTCTGATTTACGCTGCGAGCAACCTGGAGATGAGTCCCTCT 186
DB 481 GGAAGATCTCTAAGCTCTGATCTATGCTGCAACAGACTGATAGTGGGCTCCATCA 540
QY 187 CGCTTCTGATCCGCTCGGAGGAGGATTTCACTGACCATGACAGTCTGACGCT 246
DB 541 AGCTTCAGTGCAGTGCAGTGCAGACATTAATCTCTCACCATTAGCAGCTGAGTAT 600
QY 247 GAACACTGCTACTATCTACTGTCAGAACGTTTAAATACCTCCGCTTTCGACAG 306
DB 601 GAAATATGGAATTTATTTATTTTACAGTATGATGATTTCCGACGCTTCGAGG 660
QY 307 GGTACCAAGTGTGAATTAACGCTACTGCGGTGCTGCTGCTGCGGCTGATCTGCT 366
DB 661 GGTACCAAGTGTGAATTTATTTATTTTACAGTATGATGATTTCCGACGCTTCGAGG 714
QY 367 GGTGCGGCTTCTCAAGTCAACGCTGCTGCAATCCGCGCGAGCTGAAGAGCGAGGCC 426
DB 715 GCGCGGCTCTGAGGCTTCACTGTCAGTCCAGAGTCTGGAGCTGTAAGGCGCTGGGCT 774
QY 427 TCAGTCAAGTCTCTGTAAGCTAGCGCTATATTTTCTTAATTTATGATTCATGG 486
DB 775 TCAGTGAAGATCTCTGTAAGCTAGCGCTATATTTTCTTAATTTATGATTCATGG 834
QY 487 GTGCGTACGCGCGCGCGAGGCTGTAAGTATGATGATGATGATGATGATGATGATGAT 546
DB 835 ATAAACAGAGGCTGCGAGGCTGTAAGTATGATGATGATGATGATGATGATGATGATGAT 894
QY 547 AGCAACGATATACGAAATTTTAAAGACCTGTTACTATGACGCGCTGACATTCGACT 606
DB 895 GATATATTTTCAACCCGCAATTCACACAGGCAAGGCAAGCTGACATTCACCTGAC 954
QY 607 AGTACGATATCAATGAGCTCTCCAGCTGCGATGCGAGGAGCAGCGCGCTATATTGC 666
DB 955 AGCACTGCTTACATGAGCTCAACAGCTGACCAATGAGAGCTGCGGCTATTTACTGT 1014
QY 667 GCGGCTATTTT 679
DB 1015 ACCCTCTTTAT 1027

RESULT 15

US-08-875-811-42
Sequence 42; Application US/08875811

Patent No. 6045793

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: Boque, Luis

APPLICANT: Wlodawer, Alexander

TITLE OF INVENTION: Recombinant Ribonuclease Proteins

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,811

FILING DATE: 19-FEB-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588

FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/011,800

FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fatis, Susan K.

REGISTRATION NUMBER: 41,739

REFERENCE/DOCKET NUMBER: 015280-244100US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 1137 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1137

OTHER INFORMATION: /note= "SignaloncfB5"

US-08-875-811-42

Query Match 35.7%; Score 267; DB 3; Length 1137;
Best Local Similarity 63.4%; Pred. No. 2.8e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 7 GATATCCAGATGACCCATCCCGCTCTCCCTGTCGCGCTGTGGCGATAGGGTACC 66
DB 427 GACATCAAGATGACCCATCCCGCTCTCCCTGTCGCGCTGTGGCGATAGGGTACC 486
QY 67 ATACCTGCGCGCGCGAGGAAACATCTATGCGCGCTGTAAGTATCAAGTAACT 126
DB 487 TTCCTTGCAAGGAGGAGTCAGACATTAATACTATTATGCTGCTCCAGAGAAACA 546
QY 127 GGAAGAGCTCCGAACTCTGATTTACGCTGCGAGCAACCTGGAGATGAGTCCCTCT 186
DB 547 GGAAGATCTCTAAGCTCTGATCTATGCTGCAACAGACTGATAGTGGGCTCCATCA 606
QY 187 CGCTTCTGATCCGCTCGGAGGAGGATTTCACTGACCATGACAGTCTGACGCT 246
DB 607 AGCTTCAGTGCAGTGCAGTGCAGACATTAATCTCTCACCATTAGCAGCTGAGTAT 666
QY 247 GAAGACTTCTCTAAGCTCTGATCTGTCAGAACGTTTAAATCTCCGCTGATTTGAG 306
DB 667 GAAGATATGGAATTTATTTATTTTACAGTATGATGATGATGATGATGATGATGATGAT 726
QY 307 GGTACCAAGTGTGAATTAACGCTACTGCGGTGCTGCTGCTGCGGCTGATCTGCT 366
DB 727 GGTACCAAGTGTGAATTTATTTATTTTACAGTATGATGATGATGATGATGATGATGAT 780
QY 367 GGTGCGGCTTCTCAAGTCAACGCTGTCATTCGCGCGCGAGCTCAAGAGCGAGGCC 426
DB 781 GCGCGGCTCTGAGGCTTCAAGTTCAGACAGTCTGCGAGCTGAGCTGAGCGAGGCT 840
QY 427 TCAGTCAAGTCTCTGTAAGCTAGCGCTATATTTTCTTAATTTATGATTCATGG 486
DB 841 TCAGTGAAGATGCTGCAAGCTTCTGCTACACCTTTTCAGCTTACTGATGACACTG 900
QY 487 GTGCGTACGCGCGCGCGAGGCTGGAATGATGATGATGATGATGATGATGATGATGAT 546

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Db 901 ATAAACAGAGGCTGAGAGGCTCTGGACTGATGCTGCTATGATCTCGAATAGT 960
QY 547 AGCACCAGATATACGAAAAATTTAAAGACCGTGTATGATGACGGGTGACACTGACT 606
Db 961 GATACTATTTACACCCGCAATTCAACACAGCCCAACTGACTGACAGTCACTCCACC 1020
QY 607 AGTACAGTATGATGAGCTCTCCAGCTGCGATGCGAGAGACACGGCCGCTCTATTATGCG 666
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QY 667 GCGGCTATTTT 679
Db 1081 ACCCTCTTTATT 1093

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 Job time: 6177 sec


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C/Date: 12-Oct-1989 #sequence_rev1sion 12-Oct-1989 #text_change 16-Aug-1996
C/Accession: A32483
L/Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C.
A/Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells used
A/Reference number: A32483; M0ID:89273586
A/Accession: A32483
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-142 <LAR>
A/Cross-references: GB:M26463
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
I:25-108/Domain: Immunoglobulin homology <IMW>

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C|Date: 19-May-1994 #sequence-revision 26-May-1995 #text-change 21-Jan-2000
C|Accession: S40367
R|Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A|Title: Expressed human immunoglobulin chi genes and their hypermutation
A|Reference number: S40312; MUID:94080891
A|Accession: S40367
A|Status: preliminary; translation not shown
A|Status: preliminary; translation not shown
A|Molecule type: mRNA
A|Residues: 1-127 <KBL>
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68	AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerIlyse	84		
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84	rgIyThnAspPheThrIleuThrIleSerSerLeuGlnProGluAspPheA	101		
257	CTACGATTAATCTGTGACAGACGTTTAAATFACTCGCTTCCGACAGC	306		
101	IaThrTyrTyrCysGlnGlnSerTyrAsnThrProTrpPheGlyGln	117		
307	GGTACCAAGGTGGAATAAATACGTA	333		
118	GlyThrIlyValGluIleIysAsnTyr	126		


```

seq_name: p1r2:S36265

seq_documentation_block:
Ig heavy chain V region (clone alpha-MUCl-1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malingvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36265; MUID:93178448
A:Accession: S36265
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GR1>
A:Cross-references: EMBL:218846; NID:933121; PID:CAA79298.1; PID:9339900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 476.00 Length: 122
Ratio: 4.250 Gaps: 1
Percent Similarity: 91.803 Percent Identity: 76.230

alignment_block:
US-08-487-283a-8 x S36265 ..

Align seg 1/1 to: S36265 from: 1 to: 118

379 CAAGTCCAACTGTCGCAATCCGGCCGAGGTCAAGAACGAGGCGCTC 428
1 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaSer 17
429 AGTCAAGTCTCCTGTAAGCTAGCGCTATATTTTCTAATATTGGA 478
17 rValLysValSerCysLysAlaSerGlyTyrPheThrGlyTyrTyrM 34
479 TTCATGGGTGCGTCAGACCCCGCGAGGCTGAAATGATGGAGT 528
34 ethIstrpValArgGlnAlaProGlyGlnGlyLeuGlnTyrMetCylTyr 50
529 ATCTTACCGGCGCTGCTGATACCGCAATATACGAAATTTAAAGCG 578
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyAr 67
579 TGTACTATGACGCGTGACACTTGACTAGTACAGTATACATGAGCTCT 628
67 gValThrIleThrArgAspThrSerAlaSerThrAlaTyrMetGlnLys 84
629 CCAGCTGCATCGAGAGACAGCGCGCTCTATTATTTGGCGGTATT 678
84 eArLeuValArgSerGlnAspThrAlaValTyrTyrCysAlaArgAspPhe 100
679 TTTGGTCTAGCCGAATGGTATTGATGTTGGGGTCAAGAACCT 728
101 LeuSerCyl.....TyrLeuAspTyrTrpGlyGlnGlyThrLe 113
729 GGTCACTGTCCTCGAGC 744
113 uValThrValSerSer 118

seq_name: p1r2:S46393

seq_documentation_block:
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
R:FiJinL, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

```

```

A:Reference number: S46393; MUID:94254092
A:Accession: S46393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <FIG>
A:Cross-references: EMBL:231680; NID:9509786; PID:CAA83485.1; PID:91335146
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 471.50 Length: 129
Ratio: 4.210 Gaps: 2
Percent Similarity: 86.822 Percent Identity: 72.093

alignment_block:
US-08-487-283a-8 x S46393 ..

Align seg 1/1 to: S46393 from: 1 to: 129

379 CAAGTCCAACTGTCGCAATCCGGCCGAGGTCAAGAACGAGGCGCTC 428
1 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaSer 17
429 AGTCAAGTCTCCTGTAAGCTAGCGCTATATTTTCTAATATTGGA 478
17 rValLysValSerCysLysAlaSerGlyTyrPheThrGlyTyrTyrM 34
479 TTCATGGGTGCGTCAGACCCCGCGAGGCTGAAATGATGGAGT 528
34 ethIstrpValArgGlnAlaProGlyGlnGlyLeuGlnTyrMetCylTyr 50
529 ATCTTACCGGCGCTGCTGATACCGCAATATACGAAATTTAAAGCG 578
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyTyr 67
579 TGTACTATGACGCGTGACACTTGACTAGTACAGTATACATGAGCTCT 628
67 pValThrMetThrArgAspThrSerAlaSerThrAlaTyrMetGlnLys 84
629 CCAGCTGCATCGAGAGACAGCGCGCTCTATTATTTGGCGGTCT 672
84 eArLeuValArgSerGlnAspThrAlaValTyrTyrCysAlaArgAspSer 100
673 ...TATTTTTCGCTCT.....AGCCGAATGATGATTTTGA 707
101 AlaTyrTyrTyrAspSerSerGlyTyrTyrSerAlaAsnTyrTyrMetAs 117
708 TGTGGGGTCAAGAACCTGCTGCTGCTGAGC 744
117 pValTyrPylGlyGlyGlyThrThrValThrValSerSer 129

seq_name: p1r2:C30562

seq_documentation_block:
Ig heavy chain V region (27.7.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: C30562
R:Slinder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison,
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idlotype but not the antigen
A:Reference number: A30562; MUID:89110066
A:Accession: C30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SKI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

alignment_scores: Length: 122
 Quality: 467.50
 Ratio: 4.289
 Percent Similarity: 89.344 Percent Identity: 70.492

alignment_block:

US-08-487-283a-8 x C30562 ..

Align seg 1/1 to: C30562 from: 1 to: 119

```

379 GAAGTCACACGCTGGTGCATCCGCGCGAGGTCACAGACGACGAGGCTC 428
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1  GlnValGlnLeuGlnGlnSerGlyAlaGlnLeuMetLysProGlyAlaSer 17
429 ACTCAAGTGTCTCTGTAAGCTAGCGGCTATATTTTCTTAATTATGGA 478
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 rVallyslieserCysLysAlaThrGlyTyrThrPheSerSerTyrTrpI 34
479 TTCATGGGTGCGTCAGGCCCCGCGGACAGGCTGGAATGATGAGTGG 528
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 lGlnlTyrVallyslsGlnArgProGlyHisGlyLeuGlnTyrIleGly 50
529 ACTTACCCGGGCTCTGGTAGACACCGAATATACGAAATTTTAAAGCCG 578
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 lIleuPProGlySerlYserThrAsnTyrAsnGlnLysPheLysGly 67
579 TGTACTATGACGCGTGCACCTCGACTAGTACGATACGATACGAGCTCT 628
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
67 sAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeu 84
629 CGAGCTCGGATCGAGACGACGCGCTCTATTTATTCGCGGCTTATTTT 678
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
84 eSerLeuThrSerGlnuAspSerAlaValTyrTyrCysAlaArgHisTyr 100
679 TTTCGTTCTACGCCGATGTTGTTTTCGATTTTGGGGTCAAGAACCTT 728
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101 TyrGlySerSerSer.....PheAlaTyrTrpGlyGlnGlyThrIle 114
729 GGTCACTGTCCTCGAGC 744
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
114 uValThrValSerAla 119

```

seq_name: p1r2:B49047

seq_documentation_block:

Ig kappa chain V region (monoclonal strational autoantibody StrAB SA-1A) - human (fragm
 C:Species: Homo sapiens (man)
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B49047
 R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
 Eur. J. Immunol. 22, 2231-2236, 1992
 A:Title: Human monoclonal strational autoantibodies isolated from thymic B lymphocytes
 A:Reference number: A49047; MUID:92387224
 A:Accession: B49047
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-108 <VIC>
 A:Experimental source: thymic B lymphocytes
 A>Note: Sequence extracted from NCBI Backbone (NCBI:113208, NCBI:113209)
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 F:16-90/Domain: Immunoglobulin homology <IMM>

alignment_scores: Length: 108
 Quality: 466.00
 Ratio: 4.614
 Percent Similarity: 93.519 Percent Identity: 84.259

alignment_block:

US-08-487-283a-8 x B49047 ..

Align seg 1/1 to: B49047 from: 1 to: 108

```

7  GATATCCAGATGACCCAGTCCCGCTCTCCCTGTCGCGCTCTGTGGCGA 56
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1  AsplieglnMetInGlnSerProSerSerLeuSerAlaSerValGlyAs 17
57 TAGGGTCACATCACTCGCGGCGCAGGAAACATCTATGGCGGCGTGA 106
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 pArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeuA 34
107 ACTGATATCAACGTAAACCTGGGAAGCTCCGAACTCTGATTACGAT 156
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla 50
157 GCGACGAACCTGGCAGATGAGTCCCTTCGCTTCTGTGATCCGGCTC 206
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 AlaserSerLeuGlnSerGlyValProSerArgPheSerGlySerGlyse 67
207 CGGACGAGATTTCACCTGACCATCAGACAGTCTGACGCTGAAGCTTCG 256
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnuAspPheA 84
257 CTACGATTTACTGTCAGAACGTTTAAATACGCTTGACCTTTCGACAG 306
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
84 lAnThrTyrTyrCysGlnGlnSerTyrSerThrProLeuThrPheGlyGly 100
307 GGTACCAAGTGGAAATPAAACGT 330
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101 GlyThrLysValGlnIleLysArg 108

```

seq_name: p1r2:S49530

seq_documentation_block:

anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C:Accession: S49530
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A:Reference number: S48797
 A:Accession: S49530
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <MAN>
 A:Cross-references: EMBL:246348; NID:9560839; PIDN:CAA86467.1; PID:9560840
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 F:34-117/Domain: Immunoglobulin homology <IMM>

alignment_scores: Length: 126
 Quality: 465.00
 Ratio: 4.266
 Percent Similarity: 86.508 Percent Identity: 73.016

alignment_block:

US-08-487-283a-8 x S49530 ..

Align seg 1/1 to: S49530 from: 1 to: 135

```

367 GGTGGCGGTTCTCAAGTCCAACTGTCGAATCGGCGCCGAGGTCAAGAA 416
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
16 GlnAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGlnValLysIle 32
417 GCCAGGGGCTCAGTCAAGAGTCTCTGTAAGCTGACGGCTATATTTT 466
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
32 spArgValaSerValLysValSerCysLysAlaSerIleTyrThrPheT 49
467 CTAATTATTTGATTCATGAGGTGCTGACGCGCCGCGGACGAGCTGGAA 516
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
49 hrGlyTyrTyrMetHisTrpValArgGlnAlaIleProGlyGlnGlyLeu 65
517 TGGATGGGTGAGATCTTACCGGGCTCTGTGAGCAGACGGAATATACGAAA 566
   |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
66 TrpMetGlyTrpIleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnIly 82

```

```

:567 TTTTAAGACCGCTGTACTATGACCGCTGACACTTCGACTAGTACAGTAT 616
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82  sphegInglyArvalrThretrhrArspThrsrleSerThralat 99
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
617 ACATGAGACTCTCCAGCTCGATCGAGGACGAGCGCGCTATATATGCG 666
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99  ymetGuldeSerArgrleuArgrSerAspThralaValrlyrlyCs 115
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
667 GCGCGTATATTTTGGTCTAGCCCGAATGTATTTTGATGTTGGGG 716
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 AlArgrAlargrThrgly.....TyrAnTYrTrpGl 126
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
717 TCAAGACACCTGTGCTACTGTCTGAGC 744
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 yGInglyThrleuValrThrValrSer 135
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

seq_name: p1r2:E30562

seq_documentation_block:
lg heavy chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: E30562
R:Sticker, S.K.; Borden, P.; Grunezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idiootype but not the antigen-bi
A:Reference number: A30562; MUID:89110066
A:Accession: E30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SIK>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 464.50      Length: 122
Ratio: 4.261         Gaps: 1
Percent Similarity: 89.344      Percent Identity: 69.672

alignment_block:
US-08-487-283A-8 x E30562 ..

Align seg 1/1 to: E30562 from: 1 to: 119

379 CAAGTCAACTGTGCAATCCGGCGGAGGTCAAGACGAGGCGCTC 428
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1  GlhValGlnleuGlnInserGlyAlaGlnleuMetLysProGlyAlaSe 17
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
429 AGTCAAGTGTCTGTAAAGCTAGCGCTATATTTTCTAATATATGGA 478
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  ValLysIleSerLysLysAlaInrGlyTyrThrPheSerSerYrTrpI 34
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
479 TTCATGCGTGCCTGACAGCGCCCGGACAGGCGCTGAATGATGGGTGAG 528
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34  IeGlurTrpValLysGlnArgrProGlyHsGlyLeuGlnTrpIleGlyL 50
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
529 ATCTTACCGGGCTCTGTAGCACCGCAATATACGAAATTTTAAAGACG 578
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  IlAepheProGlySerGlySerThrLysTyrAsnGlnLysPheLysGly 67
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
579 TGTACTATATACCGGTGACACTTGACTAGTACAGTATACATGAGCTCT 628
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  salArThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeu 84
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
629 CGAGCCGCGCATGGAGACAGCGCGCTATATTTGCGCGCTATATTT 678
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84  eArSerLeuInrSerGlnAspSerAlaValrYrCysAlaArghIstYr 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
679 TTTGGTCTAGCCCGAATGTATTTGATGTTGGGCTCAAGAACCT 728
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

101 TyrGlySerSerSer.....PheAlaTYrTrpGlyGlnGlyThrLe 114
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
729 GGTCACTGTCTCGAGC 744
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
114 uValrThrValSerAla 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

seq_name: p1r2:S40331

seq_documentation_block:
lg kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40331
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:q441350; PIDN:CAA51109.1; PID:q441351
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 462.00      Length: 107
Ratio: 4.620         Gaps: 0
Percent Similarity: 93.458      Percent Identity: 84.112

alignment_block:
US-08-487-283A-8 x S40331 ..

Align seg 1/1 to: S40331 from: 1 to: 123

7  GATATCCAGATGACCGAGTCCCGCTCCCTGTCGCGCTGTGGCGGA 56
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  AspIleGlnMerThrGlnSerProSerSerLeuSerAlaSerValGlyAs 33
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
57  TAGGTCACCATCAGCTGCGGCGCCGACGCAAAACATCTATAGCGCGCTGA 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33  pArGValrThrIleThrCysArgrAlaSerGlnSerIleSerSerYrIleu 50
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
107 ACTGTATCAAGCTAAACCTGGGAAGCTCCGAAGCTTGATTTACGCT 156
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50  snTrpYrGlnGlnLysProGlyLysAlaProLysLeuLeuIleYrAla 66
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 GCGACGACCTCGCAGATGAGAGTCCCTTCGCTTCGCTGATCCGCGCTC 206
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  AlAserSerleuGlnInserGlyValProSerArgrPheSerIlySerGly 83
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
207 CGGACAGGATTCACCTGTGACCATCAGCAGCTGCAAGCTGAAGACTTCG 256
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83  rGlyTrhArpPheThrleuThrIleSerSerleuGlnProGlnAspPhea 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 CTACGATATACGTTCAGAACGTTTAAATACCTCCGTTGACTTTCGGACAG 306
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
100  lArThrYrYrCysGlnGlnInserTyrSerThrProArgrThrPheGlyGln 116
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
307 GGTACCAAGGTGGAATTAATA 327
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117  GlYThrLysValGlnIleLys 123
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

seq_name: p1r2:S23623

seq_documentation_block:
lg heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23623
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gill, R.W.; Defios, M.; Kozin, F.; Carson, D.A

```

J. Exp. Med. 175, 831-842, 1992
 A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
 A:Reference number: S23623; MUID:92156804
 A:Accession: S23623
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-171 <OLE>
 A:Cross-references: EMBL:X59702; NID:q32010; PIDN:CAA42223.1; PID:q32011
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IM>

alignment_scores:
 Quality: 461.00 Length: 130
 Ratio: 4.153 Gaps: 2
 Percent Similarity: 85.385 Percent Identity: 70.765

alignment_block:
 US-08-487-283A-8 x S23623 ..

Align seg 1/1 to: S23623 from: 1 to: 171

```

367 GGTGGCGGCTTCAAGTCCAACTGTGCAATCCGGCGGAGGTCAAGAA 416
|||||
16 GYALAHSSerGlnValGlnSerGlyAlaGlnValIysIy 32
|||||
417 GCCAGGGGCTCAGTCAAGTGCCTGTAAGGTAGGGCTATATTTT 466
|||||
32 SProlGlnAlaSerValIysValSerGlySerGlyTyrThrPheT 49
|||||
467 CTAATTATTGATTCATGATGCTGCTGAGGCCCGGCGAGGCGCTGAA 516
:: |||
49 hAlaTylGlnMetHisTrpValArgGlnAlaProGlyGlnGlyLeuGlu 65
|||||
517 TCGATGGGTGACATCTTACCAGGCTGTGTAGCAGCAGATATACGAAA 566
|||||
66 TrpMetGlyTyrPheIleAsnProAsnSerGlyGlyThrGlyGlyGln 82
|||||
567 TTTTAAAGACGCTTACTATGACGCGGTGACATGACCTAGTACGAT 616
|||||
82 SPheGlnGlyArgValThrLeuThrArgAspThrSerIleSerThrAla 99
|||||
617 ACATGAGAGCTCTCAGCCTCGCATCGAGACAGAGCGCTCTATTATGC 666
|||||
99 YrMetGlnLeuSerArgLeuThrSerAspSerAlaValIyTrpCys 115
|||||
667 GCG...CGTTATTTTGGTCTTACG.....CCGATTGGTATTT 704
|||||
116 AlaIleGlyTyrPheTyrAspGlySerAspLeuLysProSerAspVal 132
|||||
705 TGATGTTGGGTCAAGAACCTGTGCTACTGCTGAGC 744
|||||
132 eAspIleTrpGlyGlnGlyThrMetValThrValSerSer 145

```

seq_name: p1r2:D30562

seq_documentation_block:

Ig heavy chain V region (27.4b.2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
 C:Accession: D30562
 R:Silkder, S.K.; Borden, P.; Grunezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.
 J. Immunol. 142, 888-893, 1989
 A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
 A:Reference number: A30562; MUID:89110066
 A:Accession: D30562
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <STR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IM>

alignment_scores:
 Quality: 460.50 Length: 122
 Ratio: 4.225 Gaps: 1
 Percent Similarity: 89.344 Percent Identity: 68.852

alignment_block:
 US-08-487-283A-8 x D30562 ..

Align seg 1/1 to: D30562 from: 1 to: 119

```

379 CAACTCCAACTGTGTCATCCGGCGGAGGTCAAGAACCGAGGCGCTC 428
|||||
1 GlnValGlnLeuGlnGlnSerGlyAlaGlnLeuMetLysProGlyAla 17
|||||
429 AGTCAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTATGGA 478
|||||
17 rValLysIleSerCysLysAlaThrGlyTyrThrPheSerSerTyrTrp 34
|||||
479 TTCAATGGGTGCTGACAGGCGCGGCGAGGCGCTGATGATGATGGTGAG 528
|||||
34 lGluTrpValLysGlnArgProGlyHisGlyLeuGlnTrpIleGlyAla 50
|||||
529 ATCTTACCGGCTCTGTAGCAGCAGATATACGAAATTTTAAAGACG 578
|||||
51 lIlePheProGlySerGlySerSerAsnTyrSerGlnLysPheLysGly 67
|||||
579 TGTACTATGACGCGTGCACCTGTGACTAGTACATATACATGAGCTCT 628
|||||
67 sAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLys 84
|||||
629 CCACGCTCCGATTCGAGCAGCGCGCTCTATTATGGCGGCTATTTT 678
|||||
84 eSerLeuThrSerGlnAspSerAlaValIyTrpCysAlaArgHisTyr 100
|||||
679 TTTGGTCTTACCCCGAATTGGTATTGTGATGTGGGGTCAAGAACCT 728
|||||
101 TyrGlySerSerSer.....PheAlaTyrTrpGlyGlnGlyThrLe 114
|||||
729 GGTCACTGTCTGAGC 744
|||||
114 uValThrValSerAla 119

```

seq_name: p1r2:D33548

seq_documentation_block:

Ig heavy chain V-1 region (W1L2) - human
 C:Species: Homo sapiens (man)
 C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
 C:Accession: D33548
 R:Kripps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
 A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene e
 A:Reference number: A33548; MUID:89345575
 A:Accession: D33548
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-123 <KIP>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IM>

alignment_scores:
 Quality: 458.50 Length: 123
 Ratio: 4.168 Gaps: 1
 Percent Similarity: 89.431 Percent Identity: 72.358

alignment_block:
 US-08-487-283A-8 x D33548 ..

Align seg 1/1 to: D33548 from: 1 to: 123

```

379 CAAGTCAACTGTCGATCCGGCCGAGGTCAAGAACCCAGGGCCCTC 428
|||||
1 GlnvalGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSer 17
429 AGTCAAGGTGCTCTGTAAGCTACGCGCTATATTCTTAATTAATGGA 478
|||||
17 rValLysValSerCysGluAlaSerGlyTyrThrPheThrGlyHisTyrM 34
479 TTCATGGGTGCGTCAGACCCCGGGCAGGCGCTGGAATGATGGGTGAG 528
|||||
34 ethHisrPvalArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTyr 50
529 ATCTTACCGGCTCTGGTAGACCGCAATATACCGAAATTTTAAGACCG 578
|||||
51 IleasnProAsnSerGlyGlyThrAsnTyrAlaGluLysPheGlnGlyAr 67
579 TGTACTATGACGGGTGACACTGTACAGTATACATATACATGAGAGCT 628
|||||
67 gValThrIleThrArgAspThrSerIleAsnThrAlaTyrMetGluLeuS 84
629 CCAGCTCGCATCGAGACACAGCGCGTCTATTATTTGGCGCGCT...TAT 675
|||||
84 eArgLeuArgSerAspAspThrAlaValTyrTyrCysAlaArgAlaSer 100
676 TTTTGGTTCACCCGCAATGCTATTGATGTTGGGCTCAGAGAAC 725
|||||
101 TyrcysGlyTyrAspCysTyrTyrPhePheAspTyrTyrGlyGlnGlyTh 117
726 CCGTGCATCTGTGAGC 744
|||||
117 rLeuValThrValSerSer 123
seq_name: p1r2:PT0358

```

```

seq_documentation_block:
ig kappa chain V region (/D2.G12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C:Accession: PT0358
R:Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
J. Exp. Med. 173, 287-296, 1991
A:Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
A:Reference number: PT0352; MUID:91108325
A:Accession: PT0358
A:Molecule type: mRNA
A:Residues: 1-114 <SHE>
A:Experimental source: strain BALB/c
C:Comment: This protein is an anti-double-stranded DNA antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:20-94/Domain: immunoglobulin homology <IMM>

```

```

alignment_scores:
  Quality: 457.00      Length: 108
  Ratio: 4.570        Gaps: 0
Percent Similarity: 92.593      Percent Identity: 80.556

```

alignment_block:

US-08-487-283A-8 x PT0358 ..

Align seg 1/1 to: PT0358 from: 1 to: 114

```

7 GATATCCAGATGACCCAGTCCCTCCTGTCGCGCTCTGTGGCGCA 56
|||||
5 AspIleGlnMetThrGlnSerProAlaSerLeuSerAlaSerValGlyC1 21
57 TAGGGTCACCATCAGTCGGCGGCGAGGAAACATCATGGCGGGCGCA 106
|||||
21 urnrValThrIleThrCysGlyAlaSerGluAsnIleTyrGlyAlaLeuA 38
107 ACTGATTCACAACGTAACCTGGAAAGCTCGAAGCTTCGATTACGCT 156
|||||

```

```

38 snrTrpTyrGlnArgLysGlnGlyLysSerProGlnLeuLeuIleTyrGly 54
|||||
157 GCGAGCAACCTGGCAGATGGATGCCCTTCGCTTCTCTGATCCGCGCTC 206
|||||
55 AlaThrAsnLeuAlaAspGlyMetSerSerArgPheSerGlySerGlyse 71
207 CGGAAGGATTTCACTCTGACCATCAGCAGCTCAGCTGCAACACCTCG 256
|||||
71 rGlyArgGlnTyrSerLeuLysIleSerSerLeuHisProAspAspValA 88
257 CTACGATATTACTGTCCAGAACGTTTAAATACCTCCGTTGACTTCGACAG 306
|||||
88 lArThrTyrTyrCysGlnAsnValLeuSerAlaProTPrThrPheGlyGly 104
307 GGTACCAAGGTGGAATAAACGT 330
|||||
105 GlyThrLysLeuGlnIleLysArg 112
seq_name: p1r2:PH0954

```

```

seq_documentation_block:
ig heavy chain V region (G6+ CLJ-HEN) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0954
R:Martin, T.; Dufly, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0954
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-132 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: complementarity-determining 2
F:51-67/Region: complementarity-determining 3
F:68-98/Region: framework 3
F:99-120/Region: complementarity-determining 3

```

```

alignment_scores:
  Quality: 456.00      Length: 132
  Ratio: 4.183        Gaps: 2
Percent Similarity: 82.576      Percent Identity: 69.697

```

alignment_block:

US-08-487-283A-8 x PH0954 ..

Align seg 1/1 to: PH0954 from: 1 to: 132

```

379 CAAGTCAACTGTCGATCCGGCCGAGGTCAAGAACCCAGGGCCCTC 428
|||||
1 GlnvalGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSer 17
429 AGTCAAGGTGCTCTGTAAGCTACGCGCTATATTCTTAATTAATGGA 478
|||||
17 rValLysValSerCysLysAlaSerGlyTyrThrPheSerSerTyrAlaI 34
479 TTCATGGGTGCGTCAGACCCCGGGCAGGCGCTGGAATGATGGGTGAG 528
|||||
34 lSerTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGly 50
529 ATCTTACCGGCTCTGTGACACCGCAATATACCGAAATTTTAAGACCG 578
|||||
51 lIleIleProIlePheGlyThrAlaAsnTyrAlaGlnLysPheGlnGlyAr 67
579 TGTACTATGACCGGTGACACTTCGACTAGTACAGTATACATGAGAGCT 628
|||||
67 gValThrIleThrAlaAspLysSerThrSerThrAlaTyrMetGluLeuS 84

```

```

629 CCAGCCTGGGATCGAGACACGCCGCTATATTGCGCGT..... 672
|||
84 erSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgProHis 100
673 .....TATTTTGGTCTAGCCCGAATGGTATTT.. 705
|||||
101 AlaSerIleAspAspPheTrpSerGlyTyrTyrProAsnTyrTyrTyr 117
706 .....GATGTTGGGTCACGACACCTGTCACCTGTCGAGC 744
|||
117 rclYMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 132

```

OM of: US-08-487-283a-8 to: SwissProt_39:* out_format : pfs
Date: Jul 19, 2001 8:20 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL-frame+12p.model -DEV-xlp
-O/cgn2_1/USPRO.spool/US08487283/runat_19072001.075938.3923/app_query.fasta_1.817
-DB=swissprot_39 -QFMT=fasta -SUFFIX=tra.rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPEXT=10.000 -YGAPEXT=0.500
-DELOP=0.000 -DELEXT=7.000 -START=1 -MATRIX=blomsu62
-TRANS=trans40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOR=ext -MINLEN=0 -MAXLEN=2000000000
-USER=US08487283 -CGN1_1.56 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPHY
-WAIT -THREADS=1

Search information block:

Query: US-08-487-283a-8
Query length: 747
Database: SwissProt_39:*
Database sequences: 93435
Database length: 34255486
Search time (sec): 24.910000

score_list:

Sequence	Strid Orig	ZScore	EScore	Len	Documentation
SwissProt_39:KV1H_HUMAN	444.00	673.49	6.6e-30	108	P01600 homo sapiens (human)
SwissProt_39:KV1M_HUMAN	442.00	670.47	9.8e-30	108	P01605 homo sapiens (human)
SwissProt_39:KV1B_HUMAN	437.00	662.21	2.6e-29	117	P01743 homo sapiens (human)
SwissProt_39:HV07_MOUSE	437.00	660.68	2.7e-29	139	P01751 mus musculus (mouse)
SwissProt_39:KV1R_HUMAN	435.00	661.42	3.1e-29	108	P01610 homo sapiens (human)
SwissProt_39:KV1K_HUMAN	435.00	659.91	3.8e-29	108	P01603 homo sapiens (human)
SwissProt_39:KV1P_HUMAN	435.00	659.91	3.8e-29	108	P01608 homo sapiens (human)
SwissProt_39:KV1A_HUMAN	433.00	656.81	4.7e-29	129	P04431 homo sapiens (human)
SwissProt_39:KV1B_HUMAN	433.00	656.89	5.6e-29	108	P01594 homo sapiens (human)
SwissProt_39:KV1O_HUMAN	431.00	653.87	8.2e-29	108	P01607 homo sapiens (human)
SwissProt_39:KV1Q_HUMAN	430.00	652.36	1.0e-28	108	P01609 homo sapiens (human)
SwissProt_39:KV1C_HUMAN	429.00	650.85	1.2e-28	108	P01595 homo sapiens (human)
SwissProt_39:KV1N_HUMAN	429.00	650.85	1.2e-28	108	P01606 homo sapiens (human)
SwissProt_39:KV1G_HUMAN	428.00	649.34	1.5e-28	108	P01602 homo sapiens (human)
SwissProt_39:KV1V_HUMAN	425.00	644.81	2.6e-28	108	P01599 homo sapiens (human)
SwissProt_39:KV1E_HUMAN	423.00	641.79	3.9e-28	108	P01597 homo sapiens (human)
SwissProt_39:KV1S_HUMAN	423.00	641.79	3.9e-28	108	P01611 homo sapiens (human)
SwissProt_39:HV01_MOUSE	419.50	635.76	8.4e-28	121	P01745 mus musculus (mouse)
SwissProt_39:KV1A_HUMAN	419.00	631.50	1.1e-27	108	P01593 homo sapiens (human)
SwissProt_39:KV1C_HUMAN	418.00	631.50	1.1e-27	147	P01744 homo sapiens (human)
SwissProt_39:KV1D_HUMAN	417.50	633.58	1.1e-27	107	P01596 homo sapiens (human)
SwissProt_39:KV1X_HUMAN	413.00	625.12	2.8e-27	129	P04432 homo sapiens (human)
SwissProt_39:KV1G_HUMAN	411.00	622.97	4.0e-27	117	P23083 homo sapiens (human)
SwissProt_39:KV1E_HUMAN	408.00	619.15	7.1e-27	108	P01598 homo sapiens (human)
SwissProt_39:KV1I_HUMAN	408.00	617.03	7.3e-27	137	P01755 mus musculus (mouse)
SwissProt_39:KV1T_HUMAN	405.50	615.30	1.1e-26	109	P01612 homo sapiens (human)
SwissProt_39:KV1L_HUMAN	405.00	614.36	1.3e-26	108	P01614 homo sapiens (human)
SwissProt_39:HV12_MOUSE	401.50	608.63	2.5e-26	117	P01756 mus musculus (mouse)
SwissProt_39:HV10_MOUSE	401.00	607.65	2.8e-26	120	P01632 mus musculus (mouse)
SwissProt_39:KV1D_MOUSE	399.00	605.57	4.0e-26	108	P01536 mus musculus (mouse)
SwissProt_39:HV03_MOUSE	399.50	603.88	4.5e-26	120	P01747 mus musculus (mouse)
SwissProt_39:HV13_MOUSE	397.50	602.59	5.5e-26	117	P01757 mus musculus (mouse)
SwissProt_39:HV18_MOUSE	396.50	589.92	6.8e-26	138	P01680 mus musculus (mouse)
SwissProt_39:HV02_MOUSE	389.50	589.92	6.8e-26	140	P01746 mus musculus (mouse)
SwissProt_39:KV1S_MOUSE	387.00	587.46	4.1e-25	108	P01552 mus musculus (mouse)
SwissProt_39:KV1T_MOUSE	387.00	577.61	1.3e-24	118	P01633 mus musculus (mouse)
SwissProt_39:KV1J_MOUSE	379.00	575.38	1.9e-24	108	P01553 mus musculus (mouse)
SwissProt_39:KV1Q_MOUSE	378.00	573.88	2.3e-24	108	P01550 mus musculus (mouse)
SwissProt_39:KV1J_HUMAN	378.00	573.16	2.4e-24	117	P01602 homo sapiens (human)

SwissProt_39:KV1A_HUMAN + 376.50 570.90 3.2e-24 117 P01742 homo sapiens (human)
SwissProt_39:KV1L_HUMAN + 376.50 570.03 3.2e-24 129 P01813 homo sapiens (human)
SwissProt_39:KV1O_HUMAN + 374.00 567.51 5.1e-24 112 P01613 homo sapiens (human)
SwissProt_39:KV1B_MOUSE + 374.00 566.97 5.2e-24 119 P01808 mus musculus (mouse)
SwissProt_39:KV1J_MOUSE + 373.00 566.33 6.2e-24 108 P01643 mus musculus (mouse)

seq_name: SwissProt_39:KV1H_HUMAN

seq_documentation_block:
ID KV1H_HUMAN STANDARD: PRT: 108 AA.
AC P01600:
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein HAU): subdivision within
subgroups.";
RL Hoppe-Seiler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR, A01868; KIH0HU.
DR HSSP; P80362; IMTL.
DR InterPro; IPR003006; .
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin L region; Bence-Jones protein.

FT DOMAIN 1 24 34 FRAMEWORK 1
FT DOMAIN 2 35 49 FRAMEWORK 2
FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 2
FT DOMAIN 4 57 58 FRAMEWORK 3
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3
FT DISULFID 98 107 FRAMEWORK 4
FT NON_TER 23 88 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

alignment_scores:
Quality: 444.00 Length: 108
Ratio: 4.440 Gaps: 0
Percent Similarity: 92.593 Percent Identity: 79.630

alignment_block:
US-08-487-283a-8 x KV1H_HUMAN ..

Align seg 1/1 to: KV1H_HUMAN from: 1 to: 108

7 GATATCAGATGACCCAGTCCGCTCCCTGCGCGCTGTGGCGA 56
|||||
1 ASPILIEDIMETHTRGINSERPROSERSERLEUSERLASERVALGILYAS 17
57 TAGGTCACCATCAGCTGCGCGCCAGCGAAGAACTATGCGCGCTGA 106
|||||
17 PATGVATHTLIEHFCYSARGALASERGINSELTIESERTYRLEUS 34
4 ERTPTRYGNGINGINLYSPROGILYSLAPROGINVALLEUITYALA 50
107 ACTGATATCAGCTAACTGCGAAGCTCCGAGCTTGATTTACGTT 156
|||||
34 ERTPTRYGNGINGINLYSPROGILYSLAPROGINVALLEUITYALA 50
157 GCGACGACCTGCGACATGAGATCCCTTCGCTTCTGATCGCGCTC 206
|||||
51 ALASERLEUSERPROSERVALGILYALASERFARPHESERDILYSEGLYSE 67
207 CGAAGGATTTACATCTGTGACCATGACATGACATGACGCTGAGACTTCG 256

```

|||||
67 rGlyThrAspSerThrLeuThrIleSerSerLeuGlnProGluAspPheA 84
257 CTACGATTACTGTCAGAACGTTTAAATACCCGTTGACTTCGGCAG 306
|||||
84 lArHrTyTrCysGlnGlnAsnTyTrIleThrProThrSerPheGlyIn 100
307 GGTACCAAGGTGGAATAAAGCT 330
|||||
101 GlyThrArgValGluIleLysArg 108

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seq_name: SwissProt_39:KV1M_HUMAN

seq_documentation_block:

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ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (day/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR: A01871; K1HULY.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 6 89 FRAMEWORK 3.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

```

alignment_scores:

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Quality: 442.00 Length: 108
Ratio: 4.557 Gaps: 0
Percent Similarity: 89.815 Percent Identity: 79.630

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alignment_block:

US-08-487-283a-8 x KV1M_HUMAN

Align seg 1/1 to: KV1M_HUMAN from: 1 to: 108

```

7 GATATCGACATGACCCAGTCCCTGCTCCGCTCTGTCGGCGA 56
|||||
1 AsplIeGlnMetThrGlnSerProSerSerLeuSerValSerValGlyAs 17
457 TAGGGTCACCATCAGCTCGCGCCGACGCAAAACATCTATGCGCGCTGA 106
|||||
17 pArGValThrIleThrCysGlnAlaSerGlnAsnValAlaSnAlaTyTrLeuA 34
107 ACTGTATCAAGCTAAACCTGGGAAAGCTCCGAAGCTTTCGATTACGCT 156

```

```

|||||
34 snrTyTrGlnGlnInProGlyLeuAlaProLysLeuLeuIleTyrgly 50
157 GCGAGAACCGCGGACGATGGAGTCCTCTGCTCTGTCGTCGGCTC 206
|||||
51 lArHrTyTrArgGluAlaGlyValProSerArgPheSerGlySerGlySe 67
207 CGAACGAGTTTACTGTCAGACGTTTAAATACCTGCGTTGACTTCGGACAG 306
|||||
84 lArHrTyTrCysGlnGlnInProGlyLeuAlaProSerProThrPheGlyIn 100
307 GGTACCAAGGTGGAATAAAGCT 330
|||||
101 GlyThrLysValGluValLysArg 108

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seq_name: SwissProt_39:HV1B_HUMAN

seq_documentation_block:

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ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC EMBL: J00240; AAA52988.1; -.
DR PIR: A02024; HVHUNG.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1EF7 CRC64;

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alignment_scores:

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Quality: 437.00 Length: 102
Ratio: 4.505 Gaps: 0
Percent Similarity: 95.098 Percent Identity: 82.353

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alignment_block:

US-08-487-283a-8 x HV1B_HUMAN

Align seg 1/1 to: HV1B_HUMAN from: 1 to: 117

```

367 GGTGGCGTTCACATGTCACATCGGCAATCCGGCGCGAGGTCAAGAA 416
|||||
16 GlyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGluValLysly 32

```



```

417 GCCAGGGGCGCTCAAGAGTCCTCTGAAGCTAGCGGTATATTTT 466
|||||
32 sproglyalaserValysValSerCysLysAlaSerGlyThrPhe 49
467 CTATATTGATTCATGAGGTGCGTCAGCGCCCGGAGCGCTTGAA 516
|||||
49 snserYrTyrMetHisTrpValArgGlnAlaProGlyGlnGlu 65
517 TGGATGGGTGAGATCTTACCGGCTGTGTAGACCGAATATACGAAA 566
|||||
66 TrpMetGlyIleIleAsnProSerGlyGlySerThrSerYrAlaGln 82
567 TTTTAAAGACCGTGTACTATGAGCGCGTGCACCTTCGCTAGTACAT 616
|||||
82 spheGlnGlyArgValThrMetThrArgAspThrSerThrVal 99
617 ACATGAGCTCTCCAGCTCGCATCGAGACGAGCGCGCTATATATGC 666
|||||
99 YrMetGlnLeuSerSerLeuArgSerGlnAspThrAlaValTyrCys 115
667 GCGCGT 672
|||||
116 AlaArg 117

seq_name: SwissProt_39:HV07_MOUSE

seq_documentation_block:
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J00529; AAA38170.1; -
CC PIR: A02034; MHMS18.
CC InterPro: IPR003006; -
CC DR Pfam: PF00047; 19; 1.
CC KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 19
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DISULFID 41 115

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FT NON_TER 139 139
SQ SEQUENCE 139 AA; 13419 MW; 1B57DD4FD0C9F465 CRC64;

alignment_scores:
Quality: 437.00 Length: 127
Ratio: 4.009 Gaps: 2
Percent Similarity: 85.827 Percent Identity: 65.354

alignment_block:
US-08-487-283a-8 x HV07_MOUSE ..

Align seg 1/1 to: HV07_MOUSE from: 1 to: 139

367 GGTGGCGGTTCTCAAGTCCAACTGTCGCAATCCGCGCCGAGGTGAGAA 416
|||||
16 GlyValHisSerGlnValGlnLeuGlnProGlyAlaGlnLeuVal 32
417 GCCAGGGGCGCTCAGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTT 466
|||||
32 sproglyalaserValysValSerCysLysAlaSerGlyThrPhe 49
467 CTATATTGATTCATGAGGTGCGTCAGCGCCCGGAGCGCTTGAA 516
|||||
49 hrSerYrTrpMetHisTrpValArgGlnAlaProGlyArgGlnGlu 65
517 TGGATGGGTGAGATCTTACCGGCTGTGTAGACCGAATATACGAAA 566
|||||
66 TrpIleGlyArgIleAspProAsnSerGlyGlyThrLysYrAsnGlu 82
567 TTTTAAAGACCGTGTACTATGAGCGGTGACACTTCGACTGATACAGTAT 616
|||||
82 spheLysSerLysAlaThrLeuThrValAspLysProSerSerThrAla 99
617 ACATGAGCTCTCCAGCTCGCATCGAGACGAGCGCGCTCTTTATATGC 666
|||||
99 YrMetGlnLeuSerSerLeuThrSerGlnAspSerAlaValTyrCys 115
667 GCGCGTAT...TTTWTGGTCTTACCGCGCAATGATTTGATGTTTG 713
|||||
116 AlaArgTyrAspTyrTyrGlySerSer.....TyrPheAspYrTr 129
714 GGTCAAGAACCCGTGCTCAGTGTGAGC 744
|||||
129 pGlyGlnGlyThrThrLeuThrValSerSer 139

seq_name: SwissProt_39:KV1R_HUMAN

seq_documentation_block:
ID KV1R_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC PIR: A01876; K1HOME.
CC HSSP: P80362; 1MTL.
CC DR InterPro: IPR003006; -

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DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

alignment_scores:
Quality: 436.00 Length: 108
Ratio: 4.495 Gaps: 0
Percent Similarity: 89.815 Percent Identity: 78.704

alignment_block:
US-08-487-283a-8 x KV1R_HUMAN ..
Align seg 1/1 to: KV1R_HUMAN from: 1 to: 108

7 GATATCCAGATGACCCAGTCCCGCTCCCTGCTCCGCTCTGTGGCGCA 56
|||||
1 AspliegImethrGlnSerProserSerleuSerAlaSerValGlyAs 17
57 TAGGGTCACCATCCTCGCGCGCCAGCAAAACATCTATGGCGCGCTGA 106
|||||
17 parGValThrIleThrCysArgAlaSerGlnGlyIleArgAsnAspLeu 34
107 ACTGATCAAGTAACTCGGAAGCTCCGAAGCTCTGATTACGGT 156
|||||
34 htrpPyrglnGlnLysProGlyThrAlaProLysArgLeuIleTyrGly 50
157 GCGACGACCTGGCAGATGAGTCCCTCTGCTGCTGATCCGCGCTC 206
|||||
51 AlaThrSerleuGlnSerGlyValProserArgPheSerIleSerGly 67
207 CGGACGCGATTTCATCTGACCATCAGACATGCGACCTGGAAGACTTCG 256
|||||
67 rGlyThrGluPheThrLeuThrIleAsnSerleuGlnProGluAspPhe 84
257 CTACGATTATCTGTCAGAACGTTTAAATCTCCGTTGACTTCGGACG 306
|||||
84 lathrTyrTyrCysLeuGlnTyrSerPheProItrpInrPheGlyGln 100
307 GGTACCAAGGTGGAATAAATACGT 330
|||||
101 GlyThrLysValGluValLysArg 108

seq_name: SwissProt_39:KV1K_HUMAN

seq_documentation_block:
ID KV1K_HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION KA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA 'Shinoda T.;
RT Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker. *;
RL J. Biochem. 77:1277-1296(1975).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01869; KIHUKA.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FED5A2F4B CRC64;

alignment_scores:
Quality: 435.00 Length: 108
Ratio: 4.350 Gaps: 0
Percent Similarity: 92.593 Percent Identity: 73.148

alignment_block:
US-08-487-283a-8 x KV1K_HUMAN ..
Align seg 1/1 to: KV1K_HUMAN from: 1 to: 108

7 GATATCCAGATGACCCAGTCCCGCTCCCTGCTCCGCTCTGTGGCGCA 56
|||||
1 AspliegImethrGlnSerProserThrleuSerValSerValGlyAs 17
57 TAGGGTCACCATCCTCGCGCGCCAGCAAAACATCTATGGCGCGCTGA 106
|||||
17 parGValThrIleThrCysGluAlaSerGlnThrValleuSerTyrLeu 34
107 ACTGATCAAGTAACTCGGAAGCTCCGAAGCTCTGATTACGGT 156
|||||
34 sntrpPyrglnGlnLysProGlyLysAlaProLysleuLeuIleTyrAla 50
157 GCGACGACCTGGCAGATGAGTCCCTCTGCTGCTGATCCGCGCTC 206
|||||
51 AlaSerSerleuGlnThrGlyValProserArgPheSerGlyGlnGly 67
207 CGGACGCGATTTCATCTGACCATCAGCAGTCTGCGACCTGGAAGACTTCG 256
|||||
67 rGlyThr***PheThrPheThrIleSerSerVal***Pro*****Phe 84
257 CTACGATTATCTGTCAGAACGTTTAAATCTCCGTTGACTTCGGACG 306
|||||
84 lathrTyrTyrCysGln***TyrleuAspLeuProArgThrPheGlyGln 100
307 GGTACCAAGGTGGAATAAATACGT 330
|||||
101 GlyThrLysValAspLeuLysArg 108

seq_name: SwissProt_39:KV1P_HUMAN

seq_documentation_block:
ID KV1P_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION ROY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;

```

RT 2Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT "Cum.")
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hiltmann N., Barrnkol H.U., Hess M., Langer B., Ponsingl H.,
RA Steinmetz-Kayne M., Suter L., Matanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01874; KIHURY.
CC HSSP: P80362; IWTU.
CC InterPro: IPR003006;
DR Pfam: PF00047; 1g: 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 6 88 FRAMEWORK 3.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88 FRAMEWORK 4.
FT NON-TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

alignment_scores:
Quality: 435.00 Length: 108
Ratio: 4.485 Gaps: 0
Percent Similarity: 89.815 Percent Identity: 79.630

alignment_block:
US-08-487-283a-8 x KVIW_HUMAN ..

Align seg 1/1 to: KVIW_HUMAN from: 1 to: 108

7 GATATCCAGATGACCCAGTCCCGTCTCCGCTGCGCTGTGGCGA 56
1 AspileglnmethtglnserproserSerleuserAlaserValglys 17
57 TAGGTCACCATCACCCTGCGCGCCAGCAAAACATCTATGCGCGCTGA 106
17 pargValThrIleThrcysGlnAlaserGlnAspileserIleheleua 34
107 ACTGATATCAGCTAAACCTGGGAAAGCTCCGAAGCTTGTGATTACGGT 156
34 snrtpyrglnGlnLysProglYlsAlaProlylsleuIleTytrasp 50
157 GCGACGAACTGGCAGATGAGTCCCTTCGCTTCTGATCCGCTC 206
51 AlaserLysleuGlnAlaGlyValProserArgheserGlyThrGlyse 67
207 CGGAACGATTTCACTCTGACATCAGCATCTGACAGCTGAGACTTCG 256
67 rglYthrAspPhetThrPhetThrIleSerSerleuGlnProgluAspilea 84
257 CTACGATTAATCTGTCAGAACGTTTAATATCTCGTTCGTTGACTTCG 306
84 laethrYtrGlyCysGlnGlnPhaspasnleuProleuthrPhetGlyGly 100
307 GGTACCAAGGTGGAATAAAGCT 330
101 GlyThrLysValAspPheLysArg 108

seq_name: SwissProt_39: KVIW_HUMAN

seq_documentation_block:
ID KVIW_HUMAN STANDARD: PRT; 129 AA.
AC P04431.

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DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; Pubmed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL Nucleic Acids Res. 12:695-700(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X00965; CA25477.1; ALT-TERM.
DR PIR: A01883; KIHWRK.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006;
DR Pfam: PF00047; 1g: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 FRAMEWORK 2.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 111 119 FRAMEWORK 3.
FT DOMAIN 120 129 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 45 110 FRAMEWORK 4.
FT NON-TER 129 129 BY SIMILARITY.
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4ARC2F9 CRC64;

alignment_scores:
Quality: 434.00 Length: 107
Ratio: 4.429 Gaps: 0
Percent Similarity: 91.589 Percent Identity: 79.439

alignment_block:
US-08-487-283a-8 x KVIW_HUMAN ..

Align seg 1/1 to: KVIW_HUMAN from: 1 to: 129

7 GATATCCAGATGACCCAGTCCCGTCTCCGCTGCGCTGTGGCGA 56
23 AspileglnmethtglnserproserSerleuserAlaserValglys 39
57 TAGGTCACCATCACCCTGCGCGCCAGCAAAACATCTATGCGCGCTGA 106
39 pargValThrIleThrcysArgAlaserGlnIleSerAsrTytleua 56
107 ACTGATATCAGCTAAACCTGGGAAAGCTCCGAAGCTTGTGATTACGGT 156
56 snrtpyrglnGlnLysProglYlsAlaProlylsleuIleTytrasp 72
157 GCGACGAACTGGCAGATGAGTCCCTTCGCTTCTGATCCGCTC 206
73 AlaserSerleuGlnserGlyValThrserArgPheserGlyserGlyse 89
207 CGGAACGATTTCACTCTGACATCAGCATCTGACAGCTGAGACTTCG 256
89 rglYthrAspPhetThrIleSerSerleuGlnProgluAspilea 106

```



```
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 52
FT TURN 50 54
FT TURN 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;
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alignment_scores:
Quality: 431.00 Length: 108
Ratio: 4.537 Gaps: 0
Percent Similarity: 87.963 Percent Identity: 77.778

alignment_block:

US-08-487-283A-8 x KV10_HUMAN

Align seg 1/1 to: KV10_HUMAN from: 1 to: 108

```
7 GATATCCAGATGACCCAGTCCCTCCCTGCGCTCTGTGGCGA 56
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
57 TAGGTCACCATCACCCTGGCGGCCAGCAAAACATCTATGGCGCTGA 106
|||||
17 pArgValThrIleThrCysGlnAlaSerGlnAspIleLeuStyLeuA 34
107 ACTGGTATCAAGCTGAACCTGGGAAGCTCGAAGCTTGATTTACGCT 156
|||||
34 snTrpTyrGlnGlnThrProGlyLysAlaProLysLeuLeuIleTyrGlu 50
157 GCGACGACCTGGCAGATGAGATCCCTCTGCTGCTGATCCGGCTC 206
|||||
51 AlaSerThrLeuGlnAlaGlyValProSerArgPheSerGlySerGlySe 67
207 CGGAACGATTTCACTCTGACCATCAGCAGTCTGACGCTGAAGACTTCG 256
|||||
67 rGlyThrAspTyrThrPheThrIleSerSerLeuGlnProGlnAspIleA 84
257 CTACGATTACTCTGACGAACGTTTAAATACCTCCGTGACTTTGGACAG 306
|||||
84 lAsnTyrTyrCysGlnGlnTyrGlnSerLeuProTyrThrPheGlyGln 100
307 GGTACCAAGCTGGAATAAATACG 330
|||||
101 GlyThrLysLeuGlnIleThrArg 108
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seq_name: SwissProt_39:KV10_HUMAN

seq_documentation_block:

ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01609;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION SCM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_taxid=9606;

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RN [1]
RP SEQUENCE.
RX MEDLINE=75059271; PubMed=4435756;
RA Eulitz M., Hilschmann N.;
RT "The primary structure of a human immunoglobulin L-chain of
RT kappa-type (Bence-Jones protein scw.), II: The chymotryptic peptides
RT and the complete amino acid sequence."
RL Hoppe-Seyler's Z. Physiol.Chem. 355:842-866(1974).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR: A01875; KIHUSW.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11764 MW; 32CECDDF9644414 CRC64;
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alignment_scores:
Quality: 430.00 Length: 107
Ratio: 4.388 Gaps: 0
Percent Similarity: 91.589 Percent Identity: 77.570

alignment_block:

US-08-487-283A-8 x KV10_HUMAN

Align seg 1/1 to: KV10_HUMAN from: 1 to: 108

```
7 GATATCCAGATGACCCAGTCCCTCCCTGCGCTCTGTGGCGA 56
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
57 TAGGTCACCATCACCCTGGCGGCCAGCAAAACATCTATGGCGCTGA 106
|||||
17 pArgValThrIleThrCysGlnAlaSerGlnAspIleLeuStyLeuA 34
107 ACTGGTATCAAGCTGAACCTGGGAAGCTCGAAGCTTGATTTACGCT 156
|||||
34 snTrpTyrAspGlnLysProGlyLysAlaProArgLeuLeuIleTyrGly 50
157 GCGACGACCTGGCAGATGAGATCCCTCTGCTGCTGATCCGGCTC 206
|||||
51 AlaSerThrLeuGlnThrGlyValProSerArgPheSerGlySerGlySe 67
207 CGGAACGATTTCACTCTGACCATCAGCAGTCTGACGCTGAAGACTTCG 256
|||||
67 rGlyThrAspPheThrLeuThrIleSerThrLeuGlnProGlnAspIleG 84
257 CTACGATTACTCTGACGAACGTTTAAATACCTCCGTGACTTTGGACAG 306
|||||
84 lAsnTyrTyrCysGlnGlnTyrAspAsnValProIleThrPheGlyGln 100
307 GGTACCAAGCTGGAATAAATAA 327
|||||
101 GlyThrArgValGlnAsnLys 107
```

seq_name: SwissProt_39:KV1C_HUMAN

seq_documentation_block:

ID KV1C_HUMAN STANDARD; PRT; 108 AA.
AC P01595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

307 GGATCAAGGTGGAATAAAGCT 330
 |||||
 101 G1Ythrlvslglsu**llylsarg 108

seq_name: SwissProt_39:KVLY_HUMAN

seq_documentation_block:

ID KVLY_HUMAN STANDARD; PRT; 108 AA.

AC P80362;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, last sequence update)

DT 15-JUL-1999 (Rel. 38, last annotation update)

DE IG KAPPA CHAIN V-I REGION MAT.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RX MEDLINE=95086080; PubMed=7993911;

RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultz M.,

Solomon A., Stevens F.J., Schiffer M.;

RT "Comparison of crystal structures of two homologous proteins:

RT structural origin of altered domain interactions in immunoglobulin

RT light-chain dimers.";

RL Biochemistry 33:14848-14857(1994).

RN [2]

RP SEQUENCE OF 1-35.

RX MEDLINE=81267384; PubMed=6167731;

RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,

Popp R.A., Solomon A.;

RT "Characterization and preliminary crystallographic data on the VL-

RT related fragment of the human kappa Bence Jones protein Mat.;"

RL J. Mol. Biol. 147:185-193(1981).

CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PDB: 1WTL; 01-NOV-94.

DR InterPro: IPR003006; -.

DR Pfam: PF00047; 19; 1.

KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 35 49 FRAMEWORK 2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 57 88 FRAMEWORK 3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 98 107 FRAMEWORK 4.

FT DISULFID 23 88 BY SIMILARITY.

FT CONFLICT 30 31 TN -> SD (IN REF. 2).

FT NON_TER 108 108

SO SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

alignment_scores:

Quality: 428.00 Length: 108

Ratio: 4.367 Gaps: 0

Percent Similarity: 90.741 Percent Identity: 76.852

alignment_block:

US-08-487-283a-8 x KVLY_HUMAN ..

Align seg 1/1 to: KVLY_HUMAN from: 1 to: 108

```

7 GATATCAGATGACCGATCCGCTCCCTGCGGCTGTCGTGGGCGA 56
|||||
1 AspleglnmetnrlnglnserProserSerleuSerAlaSerValGlyAs 17
57 TAGGTCACCATCAGCTGCGGCGCCAGCAAAACATATATGCGGCGTGA 106
|||||
17 pargValThrIleThrIleThrcysargAlaSerGlnAspIleThrAsnTyVala 34
107 ACTGTATCAACGTAACCTGGGAAAGCTCCGAACCTTCTGATTACGCT 156
|||||

```

```

34 sntrPheglnGlnArgProGlyGlnAlaProLysValleuIleTyGly 50
157 GCGACGACCTGCGCAGATGAGTCGCCCTTCTGCTTCTGATCCGCTC 206
|||||
51 AlaSerIleLeuGlnThrGlyValProSerArgPheSerGlySerGlyse 67
207 CGGACGAGATTTCATCCTGACCATGACAGCTGCGACCTCGAAGACTTCG 256
|||||
67 rGlyThrAspPheThrPheThrIleSerSerLeuGlnProGlnAspIleA 84
257 CTAAGTATTACTGTCAGAACGTTTAAATACCTCCGTTGACTTTGCGACAG 306
|||||
84 lathrTyrrTyrcysGlnGlnThrAspThrLeuProLeuThrPheGlyGly 100
307 GGATCAAGGTGGAATAAAGCT 330
|||||
101 G1Ythrlvslglsu**llylsarg 108

```

seq_name: SwissProt_39:KVLYG_HUMAN

seq_documentation_block:

ID KVLYG_HUMAN STANDARD; PRT; 108 AA.

AC P01599;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, last sequence update)

DT 15-JUL-1999 (Rel. 38, last annotation update)

DE IG KAPPA CHAIN V-I REGION GAL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=75059122; PubMed=4215718;

RA laune C.J., Watanabe S., Hilschmann N.;

RT "The primary structure of a monoclonal IgM-immunoglobulin

RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of

RT kappa-type, subgroup I.";

RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).

CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S

CC MACROGLOBULIN.

DR PIR: A01867; KIHUGL.

DR HSSP: P01607; IIREI.

DR InterPro: IPR003006; -.

DR Pfam: PF00047; 19; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 35 49 FRAMEWORK 2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 57 88 FRAMEWORK 3.

FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 98 107 FRAMEWORK 4.

FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108

SO SEQUENCE 108 AA; 11814 MW; C1AD3CB0F60DF73 CRC64;

alignment_scores:

Quality: 425.00 Length: 108

Ratio: 4.381 Gaps: 0

Percent Similarity: 89.815 Percent Identity: 77.778

alignment_block:

US-08-487-283a-8 x KVLYG_HUMAN ..

Align seg 1/1 to: KVLYG_HUMAN from: 1 to: 108

```

7 GATATCAGATGACCGATCCGCTCCCTGCGGCTGTCGTGGGCGA 56
|||||
1 AspleglnmetnrlnglnserProserSerleuSerAlaSerValGlyAs 17

```

```

57 TAGGTCACCATCCTCGCGCGCCAGCAAAACATCTATGCGCGCTGA 106
|||||
17 parValThrIleIleCysArgAlaSerGlnGlyIleArgAsnAspLeu 34
|||||
107 ACTGGTATCAACGTAACCTGGGAAGCTCCCAAGCTCTGATTACGTT 156
|||||
34 htrPtyrGlnGlnLysProGlyLysAlaProLysGlnLeuIleTyrAla 50
|||||
157 GCGACGACCTGCGCAGATGAGTCCCTTCGCTCTCTGATCCGCGCTC 206
|||||
51 AlaSerAsnLeuGlnSerGlyValProSerArgPheSerGlyAla 67
|||||
207 CGGACGGAATTCACCTCTGACCATCAGCAGCTGCAAGCTGAAGACTTCG 256
|||||
67 aglyThrGlnPheThrLeuThrIleSerSerLeuGlnProGlnAspPheA 84
|||||
257 CTACGTATTAATCTCAGAACGTTTAAATACCTCCGTTGACTTCGACAG 306
|||||
84 lathrTyrrCysLeuGlnGlnAsnSerTyrProArgSerPheGlyGln 100
|||||
307 GGTACCAAGTGAATAAAACGT 330
|||||
101 GlyThrLysValGlnIleLysArg 108

```


OM of: US-08-487-283a-8 to: SPTREMBL_16.* out_format : pfs
Date: Jul 19, 2001 8:21 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framed+ -n2p.model -DEV=xlp
-O/cgml_1/USPO.spool/US08487283/runat_19072001_075938_3893/app.query.fasta_1.817
-DB=SPTREMBL_16 -OFMT=fastan -SUFFIX=tra.rspt -GAPOP=12.000
-GAPEXT=4.000 -NIMATCH=0.100 -LOOPTCL=0.000 -LOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPOP=6.000 -GAPEXT=7.000 -TGAPOP=10.000 -TGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pcp
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USR=US08487283.cgml_1.219 -ICPU=6 -ICPU=3 -LONGLOG -NO_XLPRX
-WAIT -THREADS=1

Search information block:

Query: US-08-487-283a-8
Query length: 747
Database: SPTREMBL_16.*
Database sequences: 425026
Database length: 132305027
Search time (sec): 76.780000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SP_human:Q9UL92	+	482.00	813.25	3.7e-37	124 Q9UL92 homo sapiens (human) . my
SP_human:Q9UL94	+	451.50	761.94	2.8e-34	119 Q9UL94 homo sapiens (human) . my
SP_human:Q9UL77	+	451.00	761.93	3.0e-34	108 Q9UL77 homo sapiens (human) . my
SP_human:Q9UL95	+	446.50	753.05	8.2e-34	125 Q9UL95 homo sapiens (human) . my
SP_human:Q9UL89	+	445.00	751.15	1.1e-33	116 Q9UL89 homo sapiens (human) . my
SP_liverectrate:Q9GY22	+	430.50	726.38	2.6e-32	119 Q9GY22 schistosoma japonicum
SP_human:Q9UL70	+	425.00	717.89	8.6e-32	108 Q9UL70 homo sapiens (human) . my
SP_human:Q9UL74	+	423.00	713.74	1.3e-31	118 Q9UL74 homo sapiens (human) . my
SP_human:Q9UL81	+	421.50	712.04	1.8e-31	107 Q9UL81 homo sapiens (human) . my
SP_human:Q9UL78	+	416.50	700.29	5.7e-31	157 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL79	+	407.00	687.40	4.3e-30	108 Q9UL79 homo sapiens (human) . my
SP_human:Q9UL77	+	405.00	675.33	7.3e-30	298 Q9UL77 homo sapiens (human) . my
SP_human:Q9UL78	+	397.50	668.50	3.5e-29	150 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	389.00	657.08	1.9e-28	117 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	379.00	634.12	2.0e-27	214 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	373.50	629.98	6.3e-27	117 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	371.00	629.35	7.0e-27	114 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	371.00	626.43	1.0e-26	108 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	371.00	626.27	1.1e-26	110 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	368.50	622.12	1.8e-26	109 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	368.50	622.12	1.8e-26	109 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	360.00	607.64	1.2e-25	110 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	356.00	600.94	2.8e-25	109 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	348.00	587.55	1.6e-24	107 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	342.50	578.08	5.2e-24	109 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	341.50	575.78	6.6e-24	117 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	341.50	574.81	6.6e-24	131 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	339.50	572.10	1.0e-23	121 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	334.00	561.12	3.2e-23	147 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	332.00	559.33	5.2e-23	122 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	328.00	553.29	1.2e-22	112 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	327.50	552.37	1.4e-22	113 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	326.00	549.45	1.9e-22	118 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	323.00	545.21	3.6e-22	107 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	322.50	544.44	4.0e-22	106 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	318.50	537.47	9.6e-22	109 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	315.50	531.82	1.9e-21	116 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	313.00	528.94	3.1e-21	99 Q9UL78 homo sapiens (human) . my
SP_human:Q9UL78	+	312.00	525.32	4.0e-21	124 Q9UL78 homo sapiens (human) . my

SP_mammal:Q9N0W6 + 309.00 520.24 7.7e-21 124 | Q9N0W6 oryctolagus cuniculus
SP_mammal:Q9N0W5 + 306.00 516.26 1.5e-20 109 | Q9N0W5 oryctolagus cuniculus
SP_human:Q9UL78 + 304.00 513.36 2.2e-20 103 | Q9UL78 mus musculus (mouse) . my
SP_human:Q9UL78 + 303.00 511.83 2.8e-20 101 | Q9UL78 mus musculus (mouse) . my
SP_human:Q9UL73 + 298.50 502.80 7.5e-20 119 | Q9UL73 homo sapiens (human) . my

seq_name: sp_human:Q9UL92

seq_documentation_block:

ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL; AF035022; AAD56258.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
FT NON_TER 1 124
FT NON_TER 1 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

alignment_scores: 482.00 Length: 124
Ratio: 4.342 Gaps: 1
Percent Similarity: 89.516 Percent Identity: 76.613

alignment_block:

US-08-487-283a-8 x Q9UL92 ..
Align seg 1/1 to: Q9UL92 from: 1 to: 124

379 CAAGTCCAACTGTCGATCCGCGCGGCGAGGTCAGAGCCAGGCGCTC 428
:::|||||
1 GluValGlnLeuValGlnSerGlyAlaGlnValGlnLysProGlyAla 17
429 AGTCAAGTCTCTGTAAGCTAGCGGCTATATTTTCTATATATGGA 478
|||||
17 TallylValSerGlyAlaSerGlyTyrThrPheSerSerTyrTyr 34
479 TTCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 528
:::|||||
34 echistrPalaPalaPalaPalaPalaPalaPalaPalaPalaPala 50
529 ACTTTCGCGGCTCTGTAGACACCAATATACCAAAATTTTAAAGACG 578
||| |||
51 TleasrProSerGlySerThrSerThrSerThrValAlaGlnLysPheGlnGly 67
579 TGTATATATGACGCGTGCACCTTGCATAGTACATACATACATAGTAC 628
|||||
67 gylalrMetThrArgAspThrSerThrSerThrValTyrMetGlnLys 84
629 CCAGCTGCGATCGAGACAGACGCGCTATATTTGCGCGCTATTTT 678
|||||
84 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgGlyLeu 100

```

679 TTTGGTTCTAGCCGCAATGTAT.....TTTGATCTTGGGCTGACG 722
      ::      |||      ::      |||      |||      |||
101 TTTValValValValValValValValValValValValValValVal 117
      |||      |||      |||      |||      |||      |||
723 AACCTGCTACTGCTCTGACG 744
      |||      |||      |||      |||      |||      |||
117 YThrLeuValThrValSerSer 124

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seq_name: sp_human:09UL94

seq_documentation_block:

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ID 09UL94      PRELIMINARY;      PRT;      119 AA.
AC 09UL94;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -! SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035020; AAD56256.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13644F545FAA16E CRC64;

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alignment_scores: Quality: 451.50 Length: 122
Ratio: 4.142 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 71.311

alignment_block:

US-08-487-283A-8 x 09UL94 ..

Align seg 1/1 to: 09UL94 from: 1 to: 119

```

379 CAAGTCCAGATGATGCAATCGCGCCGCGGCAAGACGACGAGCGGCTC 428
      ::::::::::::::::::::|||
1  GluValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaSer 17
      |||
429 ACTCAAGTGTCTCTGAAGTAGCGGCTATATTTTCTAATATTATGGA 478
      ::::::::::::::::::::|||
17 rValLysValSerGlyAlaSerGlyTyrThrPheThrGlyTyrTyrM 34
      |||
479 TTCAAATGGGTGCGTCAGCGCCCGGCGGAGGCGCTGGAATGATGGTGAG 528
      ::::::::::::::::::::|||
34 eHisThrValArgGlnAlaProGlyGlnGlyLeuGlnLutPheMetGlyTyr 50
      |||
529 ATCTTACCGGGCTCTGTGTCAGCAACGCAATATACGAAATTTTAAACCG 578
      |||
51 IleAsnProAsnSerTyrThrAsnTyrAlaGlnLysPheGlnGlyTyr 67
      |||
579 TGTACTATGACGCTGACACTTGCATGACATGATGATGACGCTC 628
      ::::::::::::::::::::|||
67 sValThrMetThrLysAspThrSerThrIleSerThrAlaTyrMetGlnLeu 84
      |||
629 CCAGCCTCGGATCGAGGACGACGCGCTATATTATTCGCGCGCTATTATT 678
      |||

```

```

84 eArgLeuArgSerAspAspThrAlaValTyrTyrCysAlaArg..... 98
      |||
679 TTTGGTTCTAGCCGCAATGTATTTGATTTGGGGCTGACGAAACCT 728
      |||
99 ...GlyGlyGlyArgGlyLeuThrPheAspProTyrGlyGlnGlyThrLe 114
      |||
729 GGTCACTGCTCTGACG 744
      |||
114 uValThrValSerSer 119

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seq_name: sp_human:09UL77

seq_documentation_block:

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ID 09UL77      PRELIMINARY;      PRT;      108 AA.
AC 09UL77;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -! SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035037; AAD56273.1; -.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

```

alignment_scores: Quality: 451.00 Length: 108
Ratio: 4.510 Gaps: 0
Percent Similarity: 92.593 Percent Identity: 81.481

alignment_block:

US-08-487-283A-8 x 09UL77 ..

Align seg 1/1 to: 09UL77 from: 1 to: 108

```

7 GATATCCAGATGACCCAGTCCCGCTCTCTGTCGCGCTCTGGGGCA 56
      |||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
      |||
57 TAGGGTACCATTCACCTGCGGCGCGGAGGAAACATCTATGCGCGCTCA 106
      |||
17 pArgValThrIleThrCysArgAlaSerGlnSerThrIleSerSerTyrLeuA 34
      |||
107 ACTGTATCAACGTAAACCTGGGAAGCTCGGAAGCTCTGATTTAGCGT 156
      |||
34 snTrpTyrGlnGlnLysProGlyLysAlaProAsnLeuLeuIleYrAla 50
      |||
157 CGCAGCAACCTGCGCAGATGAGATCCCTTCTGCTTCTGATCGGCTC 206
      |||
51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
      |||
207 CGGACGAGATTTCACCTGACCATTCAGACGCTGACGCTGACGCTGAC 256
      |||
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnAspPheA 84
      |||

```

257 CTACGATTAATCTGCACAGCTTTAAATACCGCTGACTTCGGACAG 306
 |||||.....:|||||
 84 lathyrtrycysglnlserlyserthrsertrphtpheglyglu 100
 |||||.....:|||||
 307 GGTACCAAGGTGGAATAAAGCT 330
 |||||.....:|||||
 101 GlyThrLysValGlnIleLysArg 108

seq_name: sp_human:Q9UL95

seq_documentation_block:

ID Q9UL95 PRELIMINARY; PRT; 125 AA.
 AC Q9UL95;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
 CC EMBL: AF035019; AAD56255.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 FT NON_TER 1 125
 FT NON_TER 1 125
 SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C23248BAC CRC64;

alignment_scores:
 Quality: 446.50 Length: 125
 Ratio: 4.096 Gaps: 1
 Percent Similarity: 87.200 Percent Identity: 69.600

alignment_block:
 US-08-487-283a-8 x Q9UL95 ..

Align seg 1/1 to: Q9UL95 from: 1 to: 125

379 CAAGTCCAATGCTGCATCCGGCGGAGTCAAGAAGCCAGGGCCTC 428
 :|||.....:|||||
 1 GluValGlnLeuValGlnSerGlyAlaValLysLysProGlyAlaSe 17
 |||||.....:|||||
 429 AGTCAAGTGCCTGTAAGCTAGCGGCTATTTTCTAATTAATGGA 478
 |||||.....:|||||
 17 ValLysValSerCysLysAlaSerGlyTrpThrPheThrGlyTrp 34
 |||||.....:|||||
 479 TTCAATGGTGGTGCAGGCCCGGCGAGGCGCTGAATGATGGTGAG 528
 :|||.....:|||||
 34 ethIstrpValarglnAlaProGlyGlnGlyLeuGlnTrpMetGlyTrp 50
 |||||.....:|||||
 529 ATCTACCGGGCTCTGTAGCAGCGAATATACGAAATTTTAAAGACG 578
 |||||.....:|||||
 51 IleAspProAsnSerGlyGlyThrAsnTyraGlnLysValGlnGlyAr 67
 |||||.....:|||||
 579 TGTACTATATACGGCTGACACTTGACTAGTACGATACATGAGACTCT 628
 |||||.....:|||||
 67 gValThrMetThrArgAspThrThrIleSerThrAlaTyrlMetGluLeuS 84
 |||||.....:|||||
 629 CCAAGCCGCGATCGAGACAGCGCGCTGATATATTCGCGCGCTATATT 678

|| |||||.....:|||||
 84 etArgLeuArgSerAspAspThrAlaValTyrrTyrcysAlaArgSerGln 100
 679 TTTGGT.....:CTAGCCCGAATGGTATTTGATGCTTTGGGCTCA 719
 |||||.....:|||||
 101 GlyGlyGlyArgGlnAlaAlaAlaGlyAspAlaPheAspIleTrpGly 117
 |||||.....:|||||
 720 AGCAACCTGTGCTACTGTCTCGAGC 744
 |||||.....:|||||
 117 nglyThrMetValThrValSerSer 125

seq_name: sp_human:Q9UL89

seq_documentation_block:

ID Q9UL89 PRELIMINARY; PRT; 116 AA.
 AC Q9UL89;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
 CC EMBL: AF035025; AAD56261.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 FT NON_TER 1 116
 FT NON_TER 1 116
 SQ SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

alignment_scores:
 Quality: 445.00 Length: 118
 Ratio: 4.320 Gaps: 1
 Percent Similarity: 87.288 Percent Identity: 73.729

alignment_block:
 US-08-487-283a-8 x Q9UL89 ..

Align seg 1/1 to: Q9UL89 from: 1 to: 116

391 GTGCAATCCGGCGCCGAGTCAAGAAGCCAGGGCCTCAAGTGTG 440
 |||||.....:|||||
 1 ValGlnSerGlyAlaGlnValLysLysProGlySerSerValLysValSe 17
 |||||.....:|||||
 441 CGTAAAGCTAGCGGCTATATTTTCTAATTAATTCGATTCAGGTGC 490
 |||||.....:|||||
 17 rcysLysAlaSerGlyGlyThrPheSerSerTyraIleIleSerTrpAla 34
 |||||.....:|||||
 491 GTGAGGCCCCGGGCGAGGCTGGAATGATGGTGGATCTTACCGGCG 540
 |||||.....:|||||
 34 rglGlnAlaProGlyGlnGlyLeuGlnTrpMetIlyArgIleIleProIle 50
 |||||.....:|||||
 541 TCTGAGACGACCAATATACGAAATTTTAAAGACGCTGCTATGAC 590
 |||||.....:|||||
 51 LeuGlyIleAlaAsnTyraGlnLysPheGlnGlyArgValThrIleTh 67
 |||||.....:|||||
 591 CGGTGACCTTGCATGACTAGTACATATACATGAGAGCTCTCCAGCTCGAT 640
 |||||.....:|||||
 67 rAlaAspLysSerThrSerThrAlaTyrlMetGluLeuSerSerLeuArgS 84

641 CGAGGACACGCGCTATTATTCGCGCGTATTATTTTGGTTCAGC 630
 |||||
 84 erGluasphrAlaValTyrCysAlaSerSerSnrtpgLy..... 98
 691 CCGAATTTGATTATTCATGATTTGGGGTCAAGAACCCGTGTCACGTCTC 740
 |||||
 99 ProTYrTrpTyrPheAspLeuTrpGlyArgGlyThrLeuValThrValSe 115
 741 GAGC 744
 |||||
 115 rSer 116

seq_name: sp_invertebrate:Q9GYZ2

seq_documentation_block:
 ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.
 AC Q9GYZ2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MONOCLONAL ANTI-IDIOtypIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigeiida; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song X.T., Feng X.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
 RT Schistosoma japonicum."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF282622; AAG01452.1; -
 FT NON_TER 1 1
 FT 119 119
 SO SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

alignment_scores:
 Quality: 430.50 Length: 122
 Ratio: 4.100 Gaps: 1
 Percent Similarity: 86.066 Percent Identity: 67.213

alignment_block:

US-08-487-283A-8 x Q9GYZ2 ..

Align seg 1/1 to: Q9GYZ2 from: 1 to: 119

379 CAAGTCCAACTGGTGCATTCGCGCGCGAGGTCAAGAACGAGCGGCTC 428
 |||||
 1 GluValGlnLeuValGlnSerGlyAlaGlnValArgLysProGlyAlaSe 17
 429 AGTCAAGTGCCTCTTAAGCTAAGCGGCTATTTTCTAATTAATGGA 478
 |||||
 17 rValArgValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrTyrM 34
 479 TTCATGGGTGGTGCAGGCGCGCGGAGGCGCTGGAATGATGGTGGAG 528
 |||||
 34 eLAsnrPValArgGlnAlaProGlyHisGlyLeuGlnTrpIleGlyTyr 50
 529 AACTTACCGGGCTCTGTAGACACCGCAATATCCGAAATTTTAAAGCCG 578
 |||||
 51 IleAsnProSerArgGlyTyrThrAsnTyrAsnGlnLysPheLysAspAr 67
 579 TGTATTATGAGCGGTGACACTGACTAGTACAGTATACATGAGGCTCT 628
 |||||
 67 gValThrMetThrThrAspLysSerPheSerThrAlaTyrMetCAspLeuA 84
 629 CCAGCGTGCATCGAGACACGCGCTATTATTCGCGCGCTATTATT 678
 |||||

84 rGSerLeuArgSerAlaAspSerAlaValTyrTyrCysAlaArgTyrTyr 100
 679 TTGGTTTACCCGGAATTGGATTGTGATTTGGGGCAAGAACCT 728
 |||||
 101AspAspHisTyrCysLeuAspTyrTrpGlyGlnGlyThrTh 114
 729 GGTCACTGTCGAGC 744
 |||||
 114 rValThrValSerSer 119

seq_name: sp_human:Q9UL70

seq_documentation_block:
 ID Q9UL70 PRELIMINARY; PRT; 108 AA.
 AC Q9UL70;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; Pubmed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.N.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035044; AAD56280.1; -
 DR HSSP; P01607; IRET.
 DR InterPro; IPR003006; -
 DR InterPro; IPR003596; -
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1 1
 FT 108 108
 SO SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

alignment_scores:
 Quality: 425.00 Length: 108
 Ratio: 4.381 Gaps: 0
 Percent Similarity: 89.815 Percent Identity: 77.778

alignment_block:

US-08-487-283A-8 x Q9UL70 ..

Align seg 1/1 to: Q9UL70 from: 1 to: 108

7 GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCGCTGTGGGGA 56
 |||||
 1 AspieGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
 57 TAGGTCACATCACCCTGCGCGCGCAGCGAACAATCTATGCGCGCTGA 106
 |||||
 17 pArgValThrIleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuA 34
 107 ACTGTATCAACGTAAACCTGGGAAGCTCCGAACCTCTGATTACGCT 156
 |||||
 34 lArtpTyrGlnGlnLysProGlyLysValProLysSerLeuIleTyrAla 50
 157 GCGAGCAACTGGCAGATGAGATCCCTCTGCTCTGATCCGGCTC 206
 |||||
 51 AlaSerThrLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
 207 CGGAAGGATTACTCTGACCATCAGAGTCTGCGAGCTGGAAGACTTCG 256
 |||||
 67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlyAspValA 84

257 CTACGATTTACTGTCCAGAACGTTTAAATTAATCCTGGTGAATTTCGGACAG 308
|||||
84 LaethrYTRYCYcglInLysTYraSseSeLaProalrghrPhneGLyPro 1008
|||
307 GGTACCAGCGTGGAATAAATTAACGT 330
|||||
101 GlythrILysLeugluILleLysarrr 108


```

157 GCGACGACCTGGCAGATGAGTCCCTTCCTTCCTGATCCGGCTC 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 AlaserThrlengInserGlyValProSerArgheserGlyserGlyse 67
207 CGGACGAGATTTCACCTCTGACATCAGACAGTCTGACCTGAGACATTCG 256
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 rGlyThraSpheThrlenThrlleserCysleuGlnSerGlnAsphea 84
257 CTACGATTAATCTGACAGACGTTTAAATACCTCGTTCAGTTCGACAG 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 lathrlyrtyrCysGlnGlnTyrtYserPheProthrhPheGlyGln 100
307 GGTACCAAGGTGGAATTAACGT 330
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 GlyThrlYsValGlnIlelysarG 108

```

seq_name: sp_rodent:Q9YF0

```

seq_documentation_block:
ID Q9YF0 PRELIMINARY; PRT; 298 AA.
AC Q9YF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CN 8 SCFV.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinozuka N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinozuka N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036341; BAA86633.1; -.
DR HSSP; P01607; IREI.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

```

alignment_scores:

Quality: 405.00 Length: 113
Ratio: 4.010 Gaps: 0
Percent Similarity: 89.381 Percent Identity: 67.257

alignment_block:

US-08-487-283a-8 x Q9YF0 ..

Align seg 1/1 to: Q9YF0 from: 1 to: 298

```

4 GCGCATATCCAGATGACCCAGTCCCTCCCTCCCTGCGGCTCTGNGG 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
172 SerAspIleuInserGlnSerProAlaserSerAlaserValGI 188
54 CGATAGGGTCACCATCAGCTGCGCGCCAGCAAGAAATCATATGCGCGC 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
188 yGlnThrlValThrlleThrcysarGlyAlaserGlyAsnIleHisnTyrl 205
104 TGAAGTGGTATCAAGCTAAACCTGGGAAGCTCCGAAGCTTCTGATTTAC 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
205 euAlatrpyrGlnGlnIlyGlnIlysserProGlnleuValTyrl 221

```

```

154 GGTGGACGACACCTGGCAGATGAGTCCCTTCCTTCCTGATCCGG 203
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
222 AsnAlalyThrlenAlaspGlyValProSerArgheserGlyserG 238
204 CTCCGGAAGGATTCACCTGACATCAGACAGTCTGACCTGAGACGAC 253
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
238 yserGlyThrlGlnTyrserleuYsIleasnSerleuGlnProGlnasp 255
254 TCGCTACGATTAATCTGACAGACGTTTAAATACCTCGTTCAGTTCGGA 303
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
255 heGlyserTyrtYrtyrCysGlnHisPheThrThrProTyrtThrhPheGly 271
304 CAGGTACCAAGGTGGAATTAACGTACTGCGGTGT 342
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
272 GlyGlyThrlYsleuGlnIlelysarGAlaAlaIagly 284

```

seq_name: sp_human:Q9Y298

```

seq_documentation_block:
ID Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor."
RL Blood 92:496-506(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AJ224083; CAA11829.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

```

alignment_scores:

Quality: 397.50 Length: 126
Ratio: 3.786 Gaps: 2
Percent Similarity: 83.333 Percent Identity: 64.286

alignment_block:

US-08-487-283a-8 x Q9Y298 ..

Align seg 1/1 to: Q9Y298 from: 1 to: 150

```

367 GGTGGGGGTTTCATGTCACATGTCGATCCGGGCGGCGAGTCAAGAA 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 GlyThrlHisAlaglnValGlnleuValGlnserGlyAlaGlnVallysl 32
417 GCGAGGGGCTCAGTCAAGTGTCTGTAAGCTAGCGGCTATATTTT 466
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 sProGlyAlaserVallyValserCyslyslValserGlyTyrlThrlent 49
467 CTAAATTATTCATTCATAGGGTGGTCAGGCCCGCGGCGAGGCTGGAA 516
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
49 hrcGlnleuProValHisTrpValGlyGlnAlaProGlylyslGlyleuGln 65

```

```

517 TGGATGGGTGAGATCTTACCGGGCTCTGTGTACACCGAATATACCGAAA 566
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 TrpValGlySerPheAspProGlnSerGlyGlnSerIleTyrAlaArgG1 82
567 TTTTAAACCGCTGTACTATATACCGCGTACACTTGACTAGTACGTAT 616
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 uphelinGlnSerValThrMetThrAlaAspThrSerThrAspIleAlat 99
617 ACATGAGCTCTCCAGCCCTGATCGAGACACGCGCGCTTATATTCG 666
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 yrmGlnGlnSerSerLeuArgSerAspAspThrAlaValIlyTyrGys 115
667 GCGCGTATTTTGTGTTCTAGCCCGAATGTGATTTTGATGTTGGG 716
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
116 Ala.....ValProAspProAsp...AlaPheAspIleThrpgl 127
717 TCACAGAACCCGTGTCACGTCTCGAGC 744
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
127 yGlnGlyThrMetValThrValSerSer 136

```

seq_name: sp_rudent:Q9QXF0

seq_documentation_block:

```

ID Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TM00NGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225171; CAB65236.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MM; DB16AD0858A47E4C CRC64;

```

alignment_scores:

```

Quality: 389.50 Length: 122
Ratio: 3.745 Gaps: 1
Percent Similarity: 85.246 Percent Identity: 58.197

```

alignment_block:

US-08-487-283A-8 x Q9QXF0 ..

Align seg 1/1 to: Q9QXF0 from: 1 to: 117

```

379 CAGATCCAACTGTCATTCGCGCCGAGTCACAGACCGAGCGCTC 428
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 GlnValGlnLeuGlnGlnSerGlyProGlnLeuValSerProGlyAla 17
429 AGTCAAGTCTCTTAAAGCTAGCGCGCTATATTTTCTAATATATGGA 478
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 rVallySerSerGlySerAlaSerGlyThrPheThrAspTyrTyrM 34
479 TTCATGGGTGCTCAGCGCCCGCGAGCGCTGATGATGATGGTGA 528
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 elyTyrVallySerGlnSerHisGlySerLeuGlnIurPrIleGlyAsp 50
529 ATCTTACCGGGCTGTGTAGACACCGAATATACGAAATTTTAAAGAC 578
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 IleAsnProAsnAsnGlyGlyThrSerTyrAsnGlnIlySphelysGly 67

```

```

579 TGTACTATAGCGCGTACACTTGACTAGTACATATATAGAGCTCT 628
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 sAlaThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuA 84
629 CCAGCGTCGATCGAGACACGCGCTCTATTTATGCGCGCTATTTT 678
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 snSerLeuThrSerGlnAspSerAlaValTyrTyrGysAlaArg..... 98
679 TTGCTGTCAGCCCGAATGTGATTTGATGTTGGGTCAAGAACCT 728
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 .....AspLysAspTyrTyrPheAspTyrTrpGlyGlnGlyThr 112
729 GGTACATGTCGAGC 744
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
112 rLeuThrValSerSer 117

```

seq_name: sp_rudent:Q9RIA5

seq_documentation_block:

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ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (wab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152371; AAD40242.1; -.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; -.
DR InterPro: IPR003600; -.
DR Pfam: PF00047; 1g; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SMART: SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MM; 52BA205FDE995E2A CRC64;

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alignment_scores:

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Quality: 379.00 Length: 221
Ratio: 2.596 Gaps: 5
Percent Similarity: 66.063 Percent Identity: 41.629

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alignment_block:

US-08-487-283A-8 x Q9RIA5 ..

Align seg 1/1 to: Q9RIA5 from: 1 to: 214

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7 GATATCCAGATGACCCAGTCCCGTCTCCCTGTCGCGCTGTGGGGA 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 AspIleGlnLeuThrGlnSerProSerSerMetThrAlaSerLeuGlyG1 17
57 TAGGGTACCATCATCTGCGCGCGCAGGAGGAAACATCTATGCGCGCTGA 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 uArgValThrIlePheThrCysLysAlaSerGlnAspIleAsnSerTyr 34
107 ACTGCTTCAACGTAACCTGGGAAAGCTCGAAGCTTCGATTATACGCT 156
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 erTrpPheGlnGlnLysProGlyLysSerProLysTyrLeuIleTyrArg 50
157 GCGACGAACTGCGCAGATGAGATCCCTTCTGCTTCTGATCCGCGCTC 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```



```
51 AlasnArgLeuValAspGlyValProSerArgPheSerGlySerGlySe 67
207 CGGACGAGATTTCACCTGACCATCAGCAGTCTGCAGCCCTGAAGACTTCG 256
      ||||| |||:|||||:|||||:|||||:|||||:|||||:|||||:
67 rGlyGlnAspTyrSerLeuThrIleSerSerLeuGlnTyrGlnAspMetG 84
257 CTACGATTACTCTCAGACGCTTTAAATACTCCGTTGACTTTCGACAG 306
      :: ||||| |||: |||: |||: |||: |||: |||: |||: |||:
84 LylIeTyrTyrCysLeuGlnTyrAspGlnPheProPheThrPheGlySer 100
307 GGTACCAAGGTGGAATAATAAAGTACTGCGCGTGGTGGTCTGTGTCGCGG 356
      ||||| |||: |||: |||: |||: |||: |||: |||: |||: |||:
101 GlyThrTyrSerLeuGlnIleLysArgAlaAspAlaIaIaProThr..... 114
357 TGCATCTGTGGTGGCGGTTCTCAAGTCCAACTGGTGCAATCCGGCGCG 406
      ||| |||: |||: |||: |||: |||: |||: |||: |||: |||:
115 .ValSerIlePheProProSerSerGlnLeuThrSerGlyGlyAla. 130
407 AGGTCAAGAGAGCCAGGGGCTCAGTCAAGTGTCTCTAAAGCTAGCGGC 456
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
131 .....SerValValCysPheLeuAsnAsn 138
457 TATATTTTCTAATATATGGAATCAATGGGTGCGTCAGCCCGCGGCA 506
      :: ||| |||: |||: |||: |||: |||: |||: |||: |||: |||:
139 PheTyrProLysAspIleAsnValLysTrp.....LysIleAs 151
507 GGGCCTGGAATGATGGGTGAGATCTTA.....CCGGGCTCTGTA 547
      :||| ||| |||: |||: |||: |||: |||: |||: |||: |||: |||:
151 pGlySerGlnArgGlnAsnGlyValLeuAsnSerTrpThrAspGlnAspS 168
548 GCACCGAATATACCGAAATTTTAAAGACCGTGTACTATGACGGGTGAC 597
      || ||| ||| |||: |||: |||: |||: |||: |||: |||: |||: |||:
168 eTyrAspSerThrTyrSerMetSerThrLeuThrLeuThrLysAsp 184
598 .....ACTTC 602
      |||||
185 GluTyrGlnArgHisAsnSerTyrThrCysGlnAlaIaThrHisLysThrSe 201
603 GACTAGTACAGTA 615
      ||||| |||: |||: |||: |||: |||: |||: |||: |||: |||:
201 rThrSerProIle 205
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alignment_scores:

Quality: 1312.00 Length: 248
 Ratio: 5.290 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-487-283A-8 x AAR77607 ..

Align seg 1/1 to: AAR77607 from: 1 to: 248

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1 ATGGCGCATATCCAGATGACCCAGTCCCTCCCTCCGCTCTGT 50
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1 MetAlaAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerVa 17
51 GGGCGATAGGGTACCACATCACCCTGGCGGCGGCAAGAAACATCTATGGCG 100
|||||
17 IGLYsPArYValThrlleThrCysGLYAlaSerGlnuAnlleTYrGLY 34
101 CGCTGACTGTATCAGCTAAACCTGGGAAAGCTCCGAGCTTGTGATT 150
|||||
34 IAlEuAnTrPYrGlnArGLYsProGLYsAlaProLYsLeuLeuIle 50
151 TACGGTGGAGACACTGGCAGATGAGAGTCCCTTCGCTTCTGTGATC 200
|||||
51 TYrGLYAlArThrAsnLeuAlaAspGLYAlProSerArGPhSeSerGLYSe 67
201 CGGCTCCGGAACGGATTTCACCTCTGACATCAGACAGCTGACGCCGAG 250
|||||
67 rGLYserGLYThrAspPheThrLeuThrlleSerSerLeuGlnProGLu 84
251 ACTTCGCTACGTATTACTGTCTCAGAAAGCTTTAAATCTCCGTTGACTTC 300
|||||
84 sPPhAlArThrTYrTYrCYsGlnAsnValLeuAsnThrProLeuThrPhe 100
301 GGACAGGGTACCAAGGTGGAATAAAGCTACTGCGCGTGTGTTCTGG 350
|||||
101 GLYGLnGLYThrLYsValGLInlleLYsArGThnGLYGLYserGL 117
351 TGGCGGTGATCTGCTGGTGGCGGTTCTCAATCCCAAGCTGTCATCCG 400
|||||
117 YGLYGLYserGLYserGLYGLYserGlnValGlnLeuValGlnSerC 134
401 GCGCGGAGTCAAGAACCGAGGCGCTCAGTCAAAAGTCTCTGTAAAGCT 450
|||||
134 YAlaGLValLYsLYsProGLYAlaSerValLYsValSerCYsLYsAla 150
451 AGCGGCTATATTTTCTAATTATTGGATTCAATGGGCTCGTCAGGCCCC 500
|||||
151 SerGLYTYrIlePheSerAsnTYrTrPleGlnTrPValAlArgGlnAlAr 167
501 CGGCGAGGCGCTCGAATGATGGTGAGATCTTACCGGCGCTCGGTAGCA 550
|||||
167 oGLYGLnGLYLeuGLInTrPMeGLYGLInlleLeuProGLYserGLYser 184
551 CCGAATATACGAAATTTTAAAGCCGTTACTACTGACGCGCTGACACT 600
|||||
184 hrgLUrTYThrGlnuSnPhelysAspArYValThrMetThrArGAspThr 200
601 TCGACTACTACAGTATACATGAGAGCTCTCCAGCTCGATCGAGAGAC 650
|||||
201 SerThrSerThrValTYrMetGLInleuSerSerLeuArGSerClnuSph 217
651 GGCGCTCATATATCGCGCGCTTATTTTGGTTCTACCCGGAATTGGT 700
|||||
217 rAlaValTYrTYrCYsAlaArGTYrPhehGlySerSerProAsnTrP 234
701 ATTTCGATGTTGGGTCAGAGACCCGTCACACTGTCGAGAC 744
|||||
234 YrPhAspValTrPGLYGLnGLYThrLeuValThrValSerSer 248
seq_name: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT: AAR77616

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seq_documentation_block:

ID AAR77616 standard; Protein: 248 AA.

XX AAR77616;

XX 15-MAR-1996 (first entry)

DE Humanised CDR-grafted 5G1.1 scFv DO12.

XX Complement C5; haemolysis; kidney; glomerulonephritis;

KW monoclonal antibody; anti-inflammatory; antibody engineering;

KW humanised antibody; complementarity determining region; CDR;

XX single chain antibody; scFv.

XX Synthetic.

FT Key Location/Qualifiers

FT Region 26..36 /label= CDR-L1

FT Region 52..58 /label= CDR-L2

FT Region 91..99 /label= CDR-L3

FT Region 152..161 /label= CDR-H1

FT Region 176..186 /label= CDR-H2

FT Region 225..237 /label= CDR-H3

XX WO9529697-A1.

PD 09-NOV-1995.

XX 01-MAY-1995; 95MO-US05688.

XX 02-MAY-1994; 94US-0236208.

PA (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

XX MPI: 1995-392923/50.

DR N-PSDB; AAT08488.

XX Treating glomerulonephritis with antibody against complement C5

PT component - to inhibit complement induced cell lysis

XX Example 11; Page 138-140; 181pp; English.

XX A humanised CDR-grafted scFv, designated 5G1.1 scFv DO12 (AAR77616),

CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.

CC The scFv can be expressed in Escherichia coli ME1 cells by subcloning

CC of encoding DNA (AAR08488) into vector pET Trc S05/Tr1. This

CC humanised, recombinant antibody retained the ability of Mab 5G1.1 to

CC block human complement C5a generation and thus to reduce glomerular

CC inflammation and kidney dysfunction associated with

CC glomerulonephritis.

alignment_scores:

Quality: 1279.00 Length: 248
 Ratio: 5.178 Gaps: 0
 Percent Similarity: 99.597 Percent Identity: 97.177

alignment_block:

US-08-487-283A-8 x AAR77616 ..

Align seg 1/1 to: AAR77616 from: 1 to: 248

17 lclglutrhvalthrllethrcysglyalasergluasnlletyrglya 34
 101 CGCTGACTGATCACTAAACCTGGGAAAGCTCCGAAGTTTCGATT 150
 34 lalenuasntprtyrglnargylsglncllylserProglinleuile 50
 151 TACGGTGCAGCAACCTGGCAGATGGATCCCTTCGCTTCCTGATC 200
 51 tyrglyAlatrhAsnleuAlaspglymetSerSerArgpheserglyse 67
 201 CGGCTCCGAGACGATTTCACTCTGCACATCAGACAGTCTGCACCTG 250
 67 rclyserglyArgIntyrrtyltyltyltyltyltyltyltyltyl 84
 251 ACTTGGCTATCTATCTGTCAGACGTTTAAATCTCCGTTGACTTC 300
 84 spvalAlatrhtrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 100
 301 GGACAGGGTACCAAGGTGGAATAAAAGTACTGGCGGTGGTCTGCG 350
 101 GlyAlaglythrltylsergluueuylsargthrclyglyltylsergl 117
 351 TGGCGGTGATCTGCTGGTGGCGGTCTCAAGTCAACTGTCGCAATCG 400
 117 ygltyltyltyltyltyltyltyltyltyltyltyltyltyltyl 134
 401 GGGCGAGGTCAAGACGGGCTCAGTCAAGTCCGCTCTTAAAGCT 450
 134 lYAladlueuetylserProglYAlaSerValtyltyltyltyltyl 150
 451 ACCGGCTATATTTTCTAATTATGATTCATGAGTGGTGGTGGTGGT 500
 151 ThrGlyTyrllepheserAsnTyrrtyrtyrtyrtyrtyrtyrtyr 167
 501 CGGCGACGGCCCTGGAAATGATGGGTGAGATCTTACCGGCTTGTA 550
 167 ocltyltyltyltyltyltyltyltyltyltyltyltyltyltyl 184
 551 CGAATATACCGAAATTTTAAAGCGGTGTACTATGACGCGTGCAC 600
 184 hglutyrthrgluasnphelysAspLysAlaIaIaPheThrAla 200
 601 TCGACTAGTACAGTATACATGAGCTCCAGCTCCAGCTCCAGTAC 650
 201 SerSerAsnThrAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 217
 651 GCGCGTCTATATGCGCGCGCTATTTTGGTCTTACGCCGAATGTGT 700
 217 rAlaValtyltyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyrtyr 234
 701 ATTTGATGTTGGGTCAAGACCTGCTCCTGCTCTGCTGACG 744
 234 yrpheAspValtrpGlyAlaGlythThrValthrValSerSer 248

seq_name: /SIDS8/6/cgdata/geneseq/AA1997.DAT:AAW26651

seq_documentation_block:

ID AAW26651 standard; Protein: 382 AA.

XX AAW26651;

XX 12-FEB-1998 (first entry)

XX Chimeric receptor hCTM01/h/zeta.

XX Cell activation; chimeric receptor; DNA delivery; CTM01; scFv;
 KW IgG1; T cell receptor zeta chain; cell proliferation; cytokine;
 KW inflammation; effector; cell differentiation; antibody secretion;
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft versus host disease; human; therapy.

XX OS Chimeric - Homo sapiens.
 XX PN MO9723613-A2.
 XX PD 03-JUL-1997.
 XX PF 23-DEC-1996; 96WO-GB03209.
 XX PR 21-DEC-1995; 95GB-0026131.
 XX PA (CLLT) CELLTECH THERAPEUTICS LTD.
 XX PI Bebbington CR, Flinney HM, Lawson ADG, Weir ANC;
 XX DR WPI, 1997-351052/32.
 XX DR N-PSDB; AAT90514.
 XX PT New DNA systems for activating cells - comprising DNA coding for a
 XX PT chimeric receptor comprising 2 or more different cytoplasmic
 XX PT signalling components.
 XX PS Disclosure; Fig 9; 90pp; English.
 XX CC This protein comprises a chimeric receptor consisting of an scFv
 XX CC engineered from anti-CD3 human antibody CTM01 linked to an
 XX CC extracellular spacer comprising the human IgG1 hinge, part of the
 XX CC extracellular region of human CD28 and 4 amino acid residues, linked
 XX CC to the transmembrane and intracellular regions of the human T cell
 XX CC receptor zeta chain. It can be expressed in host (e.g. Jurkat)
 XX CC cells using a chimeric receptor gene (see AAT90514) constructed from
 XX CC DNA cassettes encoding each component of the receptor. In a claimed
 XX CC cell activation process an effector cell is transformed with DNA
 XX CC encoding a chimeric receptor containing 2 or more different
 XX CC cytoplasmic signalling components. Also claimed is use of DNA
 XX CC encoding a recombinant chimeric receptor in a DNA delivery system.
 XX CC The DNA delivery systems can be used for the activation of cells to
 XX CC provide e.g. an increase in cell proliferation, expression of
 XX CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 XX CC of cytolytic activity, differentiation or other effector functions,
 XX CC antibody secretion, phagocytosis, tumour infiltration and/or
 XX CC increased adhesion. They can be used in the treatment of e.g.
 XX CC infectious disease, inflammatory disease, cancer, allergic/atopic
 XX CC disease, congenital disease, dermatologic disease, neurologic
 XX CC disease, transplants and metabolic/diopathic disease (claimed).
 XX CC In particular, they can be used in the treatment of rheumatoid
 XX CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 XX CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 XX CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 XX CC disease or diabetes (claimed).
 XX SQ Sequence 382 AA;

alignment_scores:

Quality: 949.50 Length: 265

Ratio: 4.220 Gaps: 4

Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:

US-08-487-283A-8 x AAW26651

Align seg 1/1 to: AAW26651 from: 1 to: 382

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 21 AsplieglnmetfthglnserProserthrleuserAlaSerValGlyAs 37
 57 TAGGTCACCATCCTGCGCGCGCGAGGAAACATCTATGCGCGG... 102
 37 pArgValthrillethrcysArgSerSerLysSerleuAsnSerAsnG 54
 103CTGAACTGATACAGCTAAACCTGGGAAAGCTCCGAG 141

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54  lyasprhrphleutyrtrpheeInlnlySProGlyLyAlaProlys 70
142 CTTCGATTTACGGTGGACGACAGACCTGGACAGATGAGTCCCTTCGCTT 191
71  LeuLeuMettyrArqMetSerAsnLeuAlaSerGlyValProSerArqPh 87
192 CTTCGATTCGGGCTCCGGAACGATTTCACTCTGACATCAAGCAGCTGTC 241
87  eSerGlySerGlySerGlyThrGluPherThrLeuThrIleSerSerLeug 104
242 AGCCTGAAGACTTCGCTACGATATCTGACAGCTTTTAATCTCCG 291
104 InProSapSpPheAlaThrTrpTyrcysMetGlnHisLeuGluTrpPro 120
292 TTGACTTTCCGACAGGATACCAAGGTGGAATAAAGCTACT..... 333
121 PheThrPheGlyGlnGlyThrLysValGluValLysArgThrGlyGly 137
334 .....GGCGGTGGTGGTCTGCTGGTGGCGGTGCAT 361
137 yGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly 154
362 CTGCTGGTGGCGGTTCTCAAGTCCACGTCGTCGTCATCCGGGCGGAGTGC 411
154 erGlyGlyGlyGlySerGlnIleGlnLeuValGlnSerGlyAlaGluVal 170
412 AAGAGCCAGGAGGCGCTCAGTCAAGATGCTCTGAAGCTACCGCTATAT 461
171 LysLysProGlySerSerValLysValSerCysLysAlaSerGlyTyrTh 187
462 TTTTCTTAATTAATGATTCATAGGGTGGCTGACGCCCGCGGAGGCC 511
187 rPheThrAspTyrTyrIleAsnTrpMetArgGlnAlaProGlyGlnGly 204
512 TGAATGATGAGGCTGAGATCTTACCGGCTGTGGTAGACCGCAATATACC 561
204 engLurTrpIleGlyTyrIleAsnProGlySerGlyAsnThrLysTyrAsn 220
562 GAAATTTTAAAGACCGTACTATGACGCGTGCACACTTGACAGACATAC 611
221 GluLysPheLysGlyAlaGlnAlaThrLeuThrValAspThrAsnThr 237
612 AGTATACATGAGCTCTCAGACCTGCGATTCGAGAGACAGCGCCGTATTT 661
237 rAlaTyrMetGluLeuSerSerLeuArgSerGluAspThrAlaPheTyrP 254
662 ATTGGCGGCGT.....TATTTTGGTCTTACGCCCAATTTGG 699
254 heCysAlaArgGluLysThrThrTyrTyrAla..... 265
700 TATTTGATGTTGGGGTCAAGAACCTGCTCACTGTCTGAGAC 744
266 ...MetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 279

seq_name: /SID8/gcgdata/geneseq/AA1997.DAT.AAM26648
seq_documentation_block:
ID AAM26648 standard; Protein; 403 AA.
XX
AC AAM26648;
XX
DT 12-FEB-1998 (first entry)
XX
DE Chimeric receptor hCTMO1/CD8/CD28.
XX
KW Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; CD8;
KW CD28; cell proliferation; cytokine; inflammation; effector;
KW cell differentiation; antibody secretion; phagocytosis;
KW tumor infiltration; adhesion; infection; cancer; allergy;
KW rheumatoid arthritis; osteoarthritis; asthma; eczema;
KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
KW psoriasis; multiple sclerosis; transplant rejection; diabetes;

```

```

KW graft versus host disease; human; therapy.
XX
OS Chimeric - Homo sapiens.
XX
PN WO9723613-A2.
XX
PD 03-JUL-1997.
XX
PF 23-DEC-1996; 96WO-GB03209.
XX
PR 21-DEC-1995; 95GB-0026131.
XX
PA (CLIT ) CELLTech THERAPEUTICS LTD.
XX
PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;
XX
DR WPI: 1997-351052/32.
XX
DR N-PSDB; AAT90511.
XX
PT New DNA systems for activating cells - comprising DNA coding for a
PS signalling components.
XX
PS Disclosure: Fig 6; 90pp; English.
XX
CC This protein comprises a chimeric receptor consisting of an scFv
CC engineered from anti-CD3 human antibody CTMO1 linked to an
CC extracellular spacer from part of human CD8 hinge, linked to the
CC extracellular and intracellular components of human CD28. It can
CC be expressed in host cells using a chimeric receptor gene (see
CC AAT90511) constructed from DNA cassettes of each component. In a
CC claimed cell activation process an effector cell is transformed with
CC DNA encoding a chimeric receptor containing 2 or more different
CC cytoplasmic signalling components. Also claimed is use of DNA
CC encoding a recombinant chimeric receptor in a DNA delivery system.
CC The DNA delivery systems can be used for the activation of cells to
CC provide e.g. an increase in cell proliferation, expression of
CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
CC of cytolytic activity, differentiation or other effector functions,
CC antibody secretion, phagocytosis, tumour infiltration and/or
CC increased adhesion. They can be used in the treatment of e.g.
CC infectious disease, inflammatory disease, cancer, allergic/atopic
CC disease, congenital disease, dermatologic disease, neurologic
CC disease, transplant and metabolic/idiopathic disease (claimed).
CC In particular, they can be used in the treatment of rheumatoid
CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
CC sclerosis, organ or tissue transplant rejection, graft-versus-host
CC disease or diabetes (claimed).
XX
SQ Sequence 403 AA;

alignment_scores:
Quality: 949.50 Length: 265
Ratio: 4.220 Gaps: 4
Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:
US-08-487-283A-8 x AAM26648 ..
Align seg 1/1 to: AAM26648 from: 1 to: 403

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21 AsplleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAs 37
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57 TAGGTCACCATCAGCTCCGCGCGCCAGCAAAACATCTATGGGCGC... 102
|||||
37 pArgValThrThrLeuThrCysArgSerSerLysSerLeuLeuHisSerAsnG 54
103 .....CTGAAGTGGTATCAAGGTAAACCTGGGAAGCTCCGAAAG 141
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54  lYAspThrPheLeuTyrTrpPheGlnGlnLysProGlyLysAlaProLys 70
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71 LeuLeuMetTyrArgMetSerAsnLeuAlaSerGlyValProSerArgph 87
192 CTTCTGGATCCGGCTCCGGAACGATTTCACTTACCATCAGACTGTC 241
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
87 eSerGlySerGlySerGlyThrGlnPheThrLeuThrIleSerSerLeuG 104
242 ACCCTGAAACACTTCGCTACGATATTACTGTCAGAACGTTTAAACTCCG 291
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
104 lnpProAspAspPheAlaThrTyrTyrCysMetGlnHisLeuGluTyrPro 120
292 TTGACTTTGGACAGGCTGACCAAGGTGGAATAAAGCTACT..... 333
121 PheThrPheGlyGlnGlyThrLysValGluValLysArgThrGlyGlyG 137
334 .....GCGCGTGTGGTCTCTGCTGCGCGGTGCAT 361
137 yGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlyGly 154
362 CTTGGTGTGGCGGCTTCTCAAGTCAACTGTCGATCCGCGCGAGCTC 411
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
154 eGlyGlyGlyGlySerGlnIleGlnLeuValGlnSerGlyAlaGluVal 170
412 AAGAACCCAGGGGCTCAGTCAAGGTGCTCTTAAGCTAGCGGCTATAT 461
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
171 lYsLysProGlySerSerValLysValSerCysLysAlaSerGlyTyrTh 187
462 TTTTTCATATATGGATTCATATGAGTGCCTCAGGCCCGCGGAGGCC 511
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187 rPheThrAspTyrTyrIleAsnTrpMetArgGlnAlaProGlyGlnGly 204
512 TGGATGATGAGTGCATCTTACCGCGGCTCTGTAGCACCAGATATACC 561
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
204 eGlnIleTrpIleGlyTrpIleAspProGlySerGlyAsnTrpLysTyrAsn 220
562 GAAATATTTAAAGACCGTGTACTATAGCCGCTGACTGCTAGTAC 611
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221 GluLysPheLysGlyArgAlaThrLeuThrValAspThrSerThrAsnTh 237
612 AGTATACATGAGAGCTCTCCAGCTCGCATCGAGACACGCGCTATAT 661
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237 rAlaTyrMetGluLeuSerSerLeuArgSerGluAspThrAlaPheTyrP 254
662 ATTGCGCGCGCT.....TATTTTTCGCTTACGCCGAATTGG 699
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254 hEcysAlaArgGluLysThrThrTyrTyrAla..... 265
700 TATTTGATGTTGGGTCAGAGAACCGTGCATGCTCTCGAGC 744
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266 ...MetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 279

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seq_name: /SID58/gcgdata/geneseq/AA1997.DAT:AAW26646

seq_documentation_block:

ID AAW26646 standard; Protein: 473 AA.

AAW26646:

12-FEB-1998 (first entry)

Chimeric receptor hCTM01/CD8/zeta.

Cell activation; chimeric receptor; DNA delivery; CTM01; scFv; CD8;
 T cell receptor zeta chain; cell proliferation; cytokine;
 inflammation; effector; cell differentiation; antibody secretion;
 phagocytosis; tumour infiltration; adhesion; infection; cancer;
 allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 psoriasis; multiple sclerosis; transplant rejection; diabetes;
 graft-versus host disease; human; therapy.

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XX OS Chimeric - Homo sapiens.
XX PN MO9723613-AA2.
XX PD 03-JUL-1997.
XX PF 23-DEC-1996; 96MO-GH03209.
XX PR 21-DEC-1995; 95GB-0026131.
XX PA (CLLT ) CELLTECH THERAPEUTICS LTD.
XX PI Bebbington CR, Flinney HM, Lawson ADG, Weir ANC;
XX DR WP1; 1997-351052/32.
XX DR N-PSDB; AAT90509.
XX PT New DNA systems for activating cells - comprising DNA coding for a
XX PT chimeric receptor comprising 2 or more different cytoplasmic
XX PT signalling components.
XX PS Disclosure; Fig 4; 90pp; English.
XX CC This protein comprises a chimeric receptor consisting of an scFv
XX CC engineered from anti-CD3 human antibody CTM01 linked to an
XX CC extracellular spacer in the form of part of human CD8 hinge, linked
XX CC to the extracellular, transmembrane and intracellular components of
XX CC the human T cell receptor zeta chain. It can be expressed in host
XX CC cells (e.g. Jurkat) using a chimeric receptor gene (see AAT90509)
XX CC constructed from DNA cassettes of each component. In a claimed
XX CC cell activation process an effector cell is transformed with DNA
XX CC encoding a chimeric receptor containing 2 or more different
XX CC cytoplasmic signalling components. Also claimed is use of DNA
XX CC encoding a recombinant chimeric receptor in a DNA delivery system.
XX CC The DNA delivery systems can be used for the activation of cells to
XX CC provide e.g. an increase in cell proliferation, expression of
XX CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
XX CC of cytolytic activity, differentiation or other effector functions,
XX CC antibody secretion, phagocytosis, tumour infiltration and/or
XX CC increased adhesion. They can be used in the treatment of e.g.
XX CC infectious disease, inflammatory disease, cancer, allergic/atopic
XX CC disease, congenital disease, dermatologic disease, neurologic
XX CC disease, transplants and metabolic/adipopathic disease (claimed).
XX CC In particular, they can be used in the treatment of rheumatoid
XX CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
XX CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
XX CC sclerosis, organ or tissue transplant rejection, graft-versus-host
XX CC disease or diabetes (claimed).
XX SQ Sequence 473 AA;

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alignment_scores:

Quality: 949.50 Length: 265
 Ratio: 4.220 Gaps: 4
 Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:

US-08-487-283A-8 x AAW26646 ..

Align seg 1/1 to: AAW26646 from: 1 to: 473

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71  LeuLeuMetTyrArgMetSerAsnLeuAlaSerGlyValProSerArgPh 87
192 CTCTGATTCGGCTCCGAGACGATTTACGTCGTGACATCCAGCATCTCC 241
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87  eSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuG 104
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seq_documentation_block:
ID   AAW26647 standard; protein; 514 AA.
XX
XX   AAW26647;
XX
XX   12-FEB-1998 (first entry)
XX
DE   Chimeric receptor hCTMO1/CD8/zeta-CD28.
XX
KW   Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; CD8;
KW   CD28; T cell receptor zeta chain; cell proliferation; cytokine;
KW   inflammation; effector; cell differentiation; antibody secretion;
KW   phagocytosis; tumor infiltration; adhesion; infection; cancer;
KW   allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
KW   inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
KW   psoriasis; multiple sclerosis; transplant rejection; diabetes;
KW   graft versus host disease; human; therapy.

```

```

XX OS Chimeric - Homo sapiens.
XX
XX PN W09723613-A2.
XX
XX PD 03-JUL-1997.
XX
XX PE 23-DEC-1996; 96WO-GB03209.
XX
XX PR 21-DEC-1995; 95GB-0026131.
XX
XX PA (CLUT ) CELLTECH THERAPEUTICS LTD.
XX
XX PI Beddington CR, Finney HM, Lawson ADG, Weir ANC;
XX
XX DR WP1: 1997-351052/32.
XX
XX DR N-PSDB; AAT90510.
XX
XX PT New DNA systems for activating cells - comprising DNA coding for a
XX PT chimeric receptor comprising 2 or more different cytoplasmic
XX PT signalling components.
XX
XX PS Disclosure; Fig 5; 90pp; English.
XX
CC This protein comprises a chimeric receptor consisting of an scFv
CC engineered from anti-CD3 human antibody CTMO1 linked to an
CC extracellular spacer in the form of part of human CD8 hinge, linked
CC to the extracellular, transmembrane and intracellular components of
CC the human T cell receptor zeta chain, fused to the intracellular
CC component of human CD28. It can be expressed in host cells (e.g.
CC Jurkat) using a chimeric receptor gene (see AAT90510) constructed
CC from DNA cassettes of each component of the receptor. In a claimed
CC cell activation process an effector cell is transformed with DNA
CC encoding a chimeric receptor containing 2 or more different
CC cytoplasmic signalling components. Also claimed is use of DNA
CC encoding a recombinant chimeric receptor in a DNA delivery system.
CC The DNA delivery systems can be used for the activation of cells to
CC provide e.g. an increase in cell proliferation, expression of
CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
CC of cytolytic activity, differentiation or other effector functions,
CC antibody secretion, phagocytosis, tumour infiltration and/or
CC increased adhesion. They can be used in the treatment of e.g.
CC infectious disease, inflammatory disease, cancer, allergic/atopic
CC disease, congenital disease, dermatologic disease, neurologic
CC disease, transplant and metabolic/idiopathic disease (claimed).
CC In particular, they can be used in the treatment of rheumatoid
CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
CC sclerosis, organ or tissue transplant rejection, graft-versus-host
CC disease or diabetes (claimed).
XX
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alignment_scores:
Quality: 949.50 Length: 265
Ratio: 4.220 Gaps: 4
Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:
US-08-487-283A-8 x AAW26647 ..
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|||||
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103 .....CTGAACGTGATCAACGTAACGTAACCTGGGAAAGCTCCGAG 141

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71 LeuLeuMetYrArMgMetSerAsnLeuAlaSerGlyValProSerArgph 87
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87 eSerGlySerGlySerGlyThrGluPheThrLeuThrLeuSerLeug 104
242 AGCCTGAGACTCGCTAGCTATCTACTGACGACGTTTAAATACCTCG 291
104 InProAspAspPheAlaThrTyrTyrIcysMetGlnHisLeuGluTyrPro 120
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334 .....GGCGGTGTTCTGTGGCGGTGAT 361
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412 AAGAGCCAGGCGGCTCAGTCAAGTCCGTAAAGCTAGCGCTATAT 461
171 LysLysProGlySerSerValLysValSerCysLysAlaSerGlyTyrTh 187
462 TTTTCTAATTAATGATTCATGCGGTGCGTACGCGCCCGGAGGCC 511
187 rPheThrAspTyrTyrIleAsnTrpMetArgGlnAlaProGlyGlnGly 204
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221 GluLysPheLysGlyArgAlaThrLeuThrValAspThrSerThrAsnTh 237
612 AGTAACATGAGACTCTCCAGCTGCGATCGAGACAGCGCGCTTATTT 661
237 rAlaTyrMetGluLeuSerSerLeuArgSerGluAspThrAlaPheTyrP 254
662 ATTCGCGCGCT.....TATTTTGTGCTTACGCCCAATTTGG 699
254 heCysAlaArgGluLysThrThrTyrTyrAla..... 265
700 TATTTGATGTTGGGTCAAGAACCTGCTACTGTCCTGCGAGC 744
266 ...MetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 279

seq_name: /SID58/gcdata/geneseq/geneseqp/AA1997.DAT:AAW26650
seq_documentation_block:
ID AAW26650 standard: Protein: 692 AA.
XX
XX AAW26650:
XX
XX 12-FEB-1998 (first entry)
XX
XX Chimeric receptor hCTMO1/GI/zeta-CD28.
XX
XX Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv;
KW IgG1; CD28; T cell receptor zeta chain; proliferation; cytokine;
KW inflammation; effector; cell differentiation; antibody secretion;
KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
KW psoriasis; multiple sclerosis; transplant rejection; diabetes;

```

```

KW graft versus host disease; human; therapy.
XX
XX OS Chimeric - Homo sapiens.
XX
XX PN WO9723613-A2.
XX
XX PD 03-JUL-1997.
XX
XX PF 23-DEC-1996; 96WO-GB03209.
XX
XX PR 21-DEC-1995; 95GB-0026131.
XX
XX PA (CLLT ) CELLTech THERAPEUTICS LTD.
XX
XX PI Bebbington CR, Finney HM, Lawson ADG, Weir ANC;
XX
XX DR WPI: 1997-351052/32.
XX
XX DR N-PSDB: AAT90513.
XX
XX PT New DNA systems for activating cells - comprising DNA coding for a
PT chimeric receptor comprising 2 or more different cytoplasmic
PT signalling components.
XX
XX PS Disclosure: Fig 8; 90pp: English.
XX
XX CC This protein comprises a chimeric receptor consisting of an scFv
CC engineered from anti-CD3 human antibody CTMO1 linked to an
CC extracellular spacer comprising the Human IgG1 hinge, CH2 and CH3,
CC linked to the transmembrane and intracellular components of the
CC human T cell receptor zeta chain, fused to the intracellular region
CC of human CD28. It can be expressed in host cells (e.g. Jurkat)
CC using a chimeric receptor gene (see AAT90513) constructed from DNA
CC cassettes encoding each component of the receptor. In a claimed
CC cell activation process an effector cell is transformed with DNA
CC encoding a chimeric receptor containing 2 or more different
CC cytoplasmic signalling components. Also claimed is use of DNA
CC encoding a recombinant chimeric receptor in a DNA delivery system.
CC The DNA delivery systems can be used for the activation of cells to
CC provide e.g. an increase in cell proliferation, expression of
CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
CC of cytolytic activity, differentiation or other effector functions,
CC antibody secretion, phagocytosis, tumour infiltration and/or
CC increased adhesion. They can be used in the treatment of e.g.
CC infectious disease, inflammatory disease, cancer, allergic/atopic
CC disease, congenital disease, dermatologic disease, neurologic
CC disease, transplant and metabolic/idiopathic disease (claimed).
CC In particular, they can be used in the treatment of rheumatoid
CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
CC sclerosis, organ or tissue transplant rejection, graft-versus-host
CC disease or diabetes (claimed).
XX
XX SO Sequence 692 AA:

alignment_scores:
Quality: 949.50 Length: 265
Ratio: 4.220 Gaps: 4
Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:
US-08-487-283A-8 x AAW26650 ..
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|||||
21 ASPIGLMETHrGlnSerProSerThrLeuSerAlaSerValGlyAs 37
57 TAGGTCACCATCAGCTCGCGCGCCGAGGAAACATCTATGGCGG... 102
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37 pArgValThrIleThrCysArgSerSerLysSerLeuLHisSerAsnG 54

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54 LysaphrhPheLeuTyrTrpPheGlnGlnLysProGlyLysAlaProLys 70
142 CTTCGTGATTTACGGTGGCAGCAACCTGGCAGATGGAGTCCCTTCGCTT 191
192 CTCTGGATCCGGCTCCGGCAACGGATTTCACCTGACCATCAGACGTCTGC 241
87 eSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuG 104
242 AGCCTGAGACCTTCGTCACGTATTCCTGACAGAGCTTTAAATACTCCG 291
104 LnPrcAspAspPheAlaThrTyrTrpCysMeGlnHisLeuGluTyrPro 120
292 TTGACTTTCGACAGGGGTACCAAGGTGGAAATTAACCTACTT 333
121 PheThrPheGlyGlnGlyThrLysValGluValLysArgThrGlyGlyGly 137
334GGCGGTGGTGCTTCTGGTGGCGGTGAT 361
137 yGlySerGlyGlyGlySerGlyGlyGlyGlyGlyGlyGlyGlyGly 154
362 CTGGTGGTGGCGGTTCCTCAATCCACATCGTGCATTCGGCGCGGAGTTC 411
154 eTrpGlyGlyGlySerGlnIleGlnLeuValGlnSerGlyAlaGluVal 170
412 AAGAACCCAGGGCGCTCAGTCAAGTGTCTGTAAAGTCAGCGGTATAT 461
171 LysLysProLysSerSerValLysValSerGlyLysAlaSerGlyTyrThr 187
462 TTTTCTAATTATTGATTCATGAGGTGTCAGGCCGCCCGGCGCAGGCC 511
187 rPheThrAspTyrTrpIleAsnTrpMetArgGlnAlaProGlyGlnGlyL 204
512 TGGAAATGGATGGGGAATCTTACCGGGCTGTGTAGCACCAATATATAC 561
204 eudLutPrpIleGlyTyrIleAspProGlySerGlyAsnThrLysTyrAsn 220
562 GAAATTTTAAAGCCGTGTACTAGTACGCGGTGACACTGCGCTGTATAC 611
221 GlnLysPheLysGlyAlaGlnAlaThrLeuThrValAspThrSerThrAsn 237
612 AGTATCATGTGAGCTCTCCACCTGCGATCGAGAGACAGCGCGTCTATT 661
237 rAlaTyrMetGlnLeuSerSerLeuArgSerGlnLysPheAlaPheTyrP 254
662 ATTGCGCGGCTTATTTTGGTTCAGCCGAATTGG 699
254 heCysAlaIleArgGlnLysThrThrTyrTyrAla 265
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seq_documentation_block:
ID AAB30693 standard; Protein; 431 AA.
XX AAB30693;
AC
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DT 02-APR-2001 (first entry)
XX
DE A fusion of single chain antibody/streptavidin.
XX
KW Streptavidin; tumour cell; cancer; adenocarcinoma;
KW hematological malignancy; hUNR-Lu-10; EGP40; EPCAM.
XX
OS Synthetic.
OS Streptomyces avidinii.
OS Homo sapiens.

XX WO200075333-A1.
PN
XX
PD 14-DEC-2000.
XX
PF 05-JUN-2000; 2000WO-US15595.
XX
PR 07-JUN-1999; 99US-0137900.
PR 03-DEC-1999; 99US-0168976.
XX
PA (NEOR-) NEORX CORP.
XX
PI Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX
DR WPI: 2001-091213/10.
XX
DR N-PSDB; AAC86562.
XX
XX
PT New vector constructs for expressing genomic streptavidin fusion
PT proteins which are useful for targeting tumour cells associated with
PT cancer, e.g. adenocarcinomas -
XX
XX
PS Example 1; Fig 10; 100pp; English.

CC The present sequence encodes a fusion of the single chain antibody
CC hnuR-JU-10 and streptavidin. The antibody binds the antigen EGFR40 or
CC EPCAM. The fusion protein is expressed using vectors of the invention.
CC The specification describes vector constructs for expressing streptavidin
CC fusion proteins. The vector comprises a first nucleic acid encoding
CC streptavidin or its functional variant operatively linked to a promoter,
CC and a cloning site for insertion of a second nucleic acid sequence
CC encoding a polypeptide to be fused with streptavidin, interspersed between
CC the promoter and the first nucleic acid sequence. Alternatively, the
CC vector construct comprises a first nucleic acid, operatively linked to a
CC promoter, encoding a polypeptide to be fused with streptavidin, and a
CC cloning site for insertion of a second nucleic acid encoding at least
CC 129 amino acids of streptavidin or its functional variant. The fusion
CC proteins are useful for targeting tumour cells, particularly tumour cells
CC associated with cancer, e.g. adenocarcinomas or hematological
CC malignancies. The vector construct is useful for expressing of
CC streptavidin fusion proteins. In particular, these are useful as tools
CC for medical diagnostics and therapeutic purposes, e.g. for detecting the
CC presence or absence of, or treating, a target site within a mammalian
CC host.

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                      Ratio: 4.201
                      Gaps: 2
Percent Similarity: 88.755 Percent Identity: 73.494
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54 snEuAspTrpTyrGlnGlnIlnTysProGlyLysGlyProIylLeuLeuIle 70
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204 snThrLysSerAspLeuSerPheGlnGlyArgValThrIleThrAlaAsp 220
598 ACTTCGATGATACATATACATATGAGACCTCCAGCTCGATCGAGAGA 647
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237 pThrAlaValTyrTyrCysSerArgGluValLeu....ThrGlyThrT 252
698 GGTATTTGATGTTGGGTCAAGAACCCGTGTCACGTCTCGAGC 744
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XX
DT 26-APR-1999 (first entry)
XX
DE H6FXscfv(CEA6)trIpbScfv(CEA6) fusion protein sequence.
XX
KW Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
KW fusion protein; ligand binding structure; toxin; enzyme; cytokine;
KW artificial antibody; pharmacokinetic; pharmacodynamic; gene therapy;
KW transfection; imaging; tumour; human; tetranectin; CEA6.
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OS Homo sapiens.
XX
PN W09856906-A1.
XX
PD 17-DEC-1998.
XX
PF 11-JUN-1998; 98WO-DK00245.
XX
PR 11-JUN-1997; 97DK-0000685.
XX
PA (ETZE/) ETZERODT M.
PA (GRAV/) GRAVERSEN N J H.

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PA (HOLT/) HOLLET T L.
PA (KAST/) KASTROP J S.
XX
PI Etzerodt M, Graversen NJH, Hollet TL, Kastrop JS;
PI Larsen IK, Nielsen BB, Thøgersen HC;
XX
DR WPI: 1999-080897/07.
XX
PT New monomer polypeptide constructs for diagnosis and therapy -
PT comprise a tetranectin trimerising structural element covalently
PT linked to at least one heterologous moiety for providing functional
PT activity
XX
PS Example 4: Fig 20: 110pp: English.
PS
XX
CC The invention relates to the design of trimeric polypeptides using
CC polypeptide structural elements derived from the tetranectin protein
CC family. The trimeric polypeptides constructed as a monomer polypeptide
CC construct comprise at least one tetranectin trimerising structural
CC element (TTSE) which is covalently linked to at least one heterologous
CC moiety, the TTSE being capable of forming a stable complex with 2 other
CC TTSEs, with the proviso that the heterologous moiety is different from
CC any of the fusion proteins CIH6FXTN123, H6FXTN12, H6FXTN23
CC (AAW94261 to AAW94264). The TTSE can be used for the construction of
CC conjugates with heterologous moieties such as a ligand binding
CC structure, a toxin, a detectable label, an in situ activatable substance,
CC an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer,
CC a photo cross-linking agent, or a group facilitating conjugation of the
CC monomer polypeptide construct to a target. They can be used as vehicles
CC for assembling antibody fragments into oligomeric or multivalent
CC entities for generating chimeric artificial antibodies having
CC preselected pharmacokinetic and/or pharmacodynamic properties. The
CC constructs can be used for targeted gene therapy involving selective
CC delivery of the material for transfection or infection of the specific
CC population of cells. They can also be used for delivering a substance to
CC a cell or tissue or for delivering an imaging or toxin-conjugated
CC antibody to a tumour. They can also be used for prevention or treating a
CC disease or for diagnosis. The TTSE provides a stable structure which can
CC act as a vehicle for a wide variety of conjugates. The present sequence
CC represents a H6FXscfv(CEA6)trIpbScfv(CEA6) fusion protein sequence
CC encoded by the plasmid pHEFXscfv(CEA6)trIpbScfv(CEA6).
XX
SQ Sequence 592 AA:

```

alignment_scores:

Quality:	858.50	Length:	304
Ratio:	3.956	Gaps:	4
Percent Similarity:	71.382	Percent Identity:	59.539

alignment_block:

```

US-08-487-283A-8 x AAW94269 ..
Align seg 1/1 to: AAW94269 from: 1 to: 592
4 GCCGATATCCAGATGACCCAGTCCCGCTCCGCTGCGCGCTGTGG 53
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
154 SerAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerIleG 170
54 CGATAGGCTCACCATGACCTGCGCGCGCACCGAAACATGTATGCGCGC 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
170 yAspArgValThrIleThrCysArgAlaSerGlnGlyIleTyrHisTrpL 187
104 TGAACGTGATACAGCTAAACCTGGGAAGCTCGAAGCTTGATTAAC 153
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
187 euAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyr 203
154 GGTGCGACGAACCTGGCAGATGAGTCCCTTCGCTTCTGTGATCCGG 203
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
204 LysAlaSerSerLeuAlaSerGlyAlaProSerArgPheSerGlySerG 220
204 CTCGGAACGATTTCACTGACCATCAGACGTCGTGACGCTGAAAGCT 253
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

220 ySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnProAspAsp 237
234 TCAGTACGATTAATCTGTCAGAACGTTTAAATACCTGCTGACTTCGGA 303
    |||||
237 heAlaThrIleTyrTrpCysGlnGlnTyrSerAsnTyrProLeuThrPheGly 253
304 CAGGCTACCAAGGTGGAATAAAGCTACTGCGCGTGTGCT ..... 345
    |||||
254 GlyGlyThrIleLeuGlnIleLeuSerArgAlaAlaGlnGlnIleLeuI 270
346 TCCTGGTGGCGGTGATCTGCTGCTGCTGCT ..... 372
    |||||
270 eSerGlnGlnIleAspLeuAsnGlyAlaGlyThrGlnProProThrGlnLysp 287
372 ..... 372
287 rOLysLysIleValAsnAlaLysLysAspValValAsnThrLysMetPhe 303
372 ..... 372
304 GlnGlnLeuLysSerArgLeuAspThrLeuAlaGlnGlnValAlaLeuIle 320
373 .....GTTCTCAAGTCCAACTGCTGCAAT 397
320 uLysGlnGlnAlaLeuGlnThrGlySerGlnValGlnLeuGlnGlns 337
398 CCGCGCGCCAGGTCAAGAACCCGCGCTCACTCAAGTCTCTGTA 447
    |||||
337 eRcGlyAlaIleValLysLysProGlySerSerValLysValSerCysLys 353
448 GCTAGCGGCTAATATTTTCTAATTAATGATTCATGCGTGCAGGC 497
    |||||
354 AlaserGlyGlyThrPheSerAsnSerProIleAsnThrPheuArgGlnAl 370
498 CCGCGCGCCAGGCGCTGCAATGATGCGTGAATCAACGCGCTGTGTA 547
    |||||
370 aProGlyGlnGlyLeuGlnIleTyrMetGlySerIleIleProSerPheGly 387
548 GCACCGAATATACCGAAATTTAAAGACCGTGTACTATGACGCGGAC 597
    |||||
387 hAlaAsnTyrAlaGlnIleLysPheGlnGlyArgLeuThrIleThrAlaAsp 403
598 ACTTGACTAGTACATATACATGAGCTCTCCAGCTCGCATCGAGGA 647
    |||||
404 GluSerThrSerThrAlaTyrMetGlnLeuSerSerLeuArgSerGlnAs 420
648 CACGCGCGCTATTAATGCGCGGCTATTTTGTGCTACGCCCAAT 696
    |||||
420 pThrAlaValIleTyrTrpCysAla.....GlyArgSerHisAsn 433
697 .....TGTATTTTGTATGATTTGGGTCAAGAACCTGTGTC 732
    |||||
433 yGlnLeuIleTyrTrpTyrMetAspValIlePheGlyGlnGlyThrMetVal 449
733 ACTGTCGTCGAC 744
    |||||
450 ThrValSerSer 453

```

seq_name: /SIDS8/gcdata/geneseq/geneseq/AA1992.DAT:AA20185

seq_documentation_block:

ID_AA20185 standard; peptide; 271 AA.

AC_AA20185:

DT 15-APR-1992 (first entry)

DE Sequence of the shortened hinge version of the B7.3 single chain Fv hinge.

XX Fv fragment; in vivo diagnosis; therapy; antibody.

KW Home sapiens.

```

XX XX WO9119739-A.
PN XX
XX XX 26-DEC-1991.
PD XX
XX XX
PF 11-JUN-1991; 91WO-GB00935.
PR XX
XX 11-JUN-1990; 90GB-0012995.
PR XX
XX (CELL-) CELTECH LTD.
PA
XX King DJ, Mountain A, Owens RJ, Yarranton GT;
PI
XX WPI; 1992-024365/03.
DR
XX N-PSDB; AAQ20381.
XX
PT New multivalent antigen-binding proteins - comprise Fv fragment
PT linked to at least 1 other Fv fragment spacer and useful for
PT in-vivo diagnosis or therapy
XX
XX PS
XX Example; Fig 5; 54pp; English.
XX
CC The bivalent antigen-binding protein B7.3 Fv (AA20184) is an example
CC of the antigen-binding proteins of the invention. They comprise a
CC first Fv fragment bound to at least one other Fv fragment by a
CC linker which keeps the Fv fragment apart. The connecting structure
CC of AA20184 comprises a joining sequence derived from a human IgG1
CC domain linked to a complete human IgG4 hinge region. AA20185 is the
CC sequence of the shortened hinge version of the B7.3 single chain Fv
CC hinge.
XX
SQ Sequence 271 AA:

```

alignment_scores:

Quality:	857.50	Length:	247
Ratio:	4.123	Gaps:	2
Percent Similarity:	84.211	Percent Identity:	66.397

alignment_block:

US-08-487-283A-8 x AA20185 ..

Align seg 1/1 to: AA20185 from: 1 to: 271

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4 GCCGATATCCAGATGATGACCCAGTCCCGTCGTCGCGCTGTGGG 53
    |||||
22 AlaAspIleGlnMetThrGlnSerProAlaSerLeuSerValSerValG 38
54 CGATAGGCTCACATCACCTCGCGCGCCAGCGAAACAATCATAGCGCGC 103
    |||||
38 yGlnThrValThrIleThrCysArgAlaSerGlnAsnIleTyrSerAsn 55
104 TGACTGGTATCAACGTAACCTGGGAAGCTCCGAACTTGTGTTTAC 153
    |||||
55 euAlaTyrPyrGlnGlnIleLysGlnGlyLysSerProGlnLeuValTyr 71
154 GGTGCGAGCACTGCGAGATGAGATGCTCTGCTGCTGCTGCTGCTGCGG 203
    |||||
72 AlaAlaThrAsnLeuAlaAspGlyValProSerArgPheSerGlySerG 88
204 CTCGGAACGATTTTCACTCTGACCATGACAGAGTCTGACGCTGAAGACT 253
    |||||
88 ySerGlyThrGlnTyrSerLeuLysIleAsnSerLeuGlnSerGlnAsp 105
254 TCAGTACGATTAATCTGTCAGAACGTTTAAATACCTGCTGACTTCGGA 303
    |||||
105 heGlySerTyrTrpCysGlnIleAspThrPheGlyThrProTyrThrPheGly 121
304 CAGGCTACCAAGGTGGAATAAAGCTACTGCGCGTGTGCTGCTGCTGCG 353
    |||||
122 GlyIleThrIleLeuGlnIleLysArg...GlyIleGlyIleGlySerGlyG 137
354 CGTGGATCTGTGTGGCGGTTCTCAAGTCCAACTGCTGCAATCCGCGG 403

```

137 yglglysergylglyglyserglnvalglnleuglninserapa 154
 404 CCGAGGTCAAGAACCCGAGGCTCAAGTCAAGTCTGTAAGCTAGC 453
 154 lacluleuvallysproglyalaservallysercyslyalaser 170
 454 GGTATATTTTCTATATTTGATTCATGGGTGGTCAAGCCCGG 503
 171 glytyrthrphethrasphialailehistrpalalysglnlysprog 187
 504 GCGAGGCTGATGATGGTGGATCTTACCGGCTGGTGGTGGACCG 553
 187 ugnllyleuglnutprileglytyrileserproglyasnapsrpiele 204
 554 AATATACCGAAATTTTAAAGACCGTGTACTATAGCCGCTGACCTTCG 603
 204 ystrasnnglnulyspnelysglylysalathrleuthralaasplys 220
 604 ACTAGTACACTATACATGAGCTCTCCAGCTCGATCGAGACACGGC 653
 221 SerSerThrAlaTyMetGlnLeuAsnSerleuthrSerGlnAspSerAl 237
 654 CGTCTATTATGGCGGTATTTTGGTGTCTAGCCCGAATGGTAT 703
 237 aValtyrPheCysLysArgSerTyTyTgLYHs..... 248
 704 TTGATGTTGGGTCAAGAACCTGCTGACCTGCTGACG 744
 249TtpglyglnglyThrThrleuthrValSerSer 259
 seq_name: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:AA91026
 seq_documentation_block:
 ID AA91026 standard; Protein; 436 AA.
 AC AA91026;
 DT 05-SEP-2000 (first entry)
 DE Apoptobody3sc fusion protein SEQ ID NO:8.
 KW Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion gene;
 KW medical; pharmaceutical; pharmacological; biochemical.
 OS Homo sapiens.
 OS Synthetic.
 PN JP2000102389-A.
 PD 11-APR-2000.
 PE 29-SEP-1998; 98JP-0291441.
 PR 29-SEP-1998; 98JP-0291441.
 PA (HAGI/) HAGIMARA Y.
 PA (HAGI/) HAGIMARA H.
 DR WPI; 2000-332086/29.
 DR N-PSDB; AAA39167.
 PT Causing apoptosis comprises transfecting fused gene to cell and
 PT reacting cell with idiotype antibody -
 PS Disclosure: Page 8-9; 10pp; Japanese.
 CC The present invention describes a method for causing apoptosis in which
 CC a fused gene consisting of a gene participating to apoptosis and a gene
 CC encoding at least the variable region of anti-idiotype antibody is
 CC transfected to a cell to express the fused gene and then an idiotype
 CC antibody is reacted with the expressed cell. The method is useful in
 CC medical, pharmaceutical, pharmacological and biochemical fields. The

CC present sequence represents a fusion protein designated apoptobody3sc.
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 436 AA;
 alignment_scores:
 Quality: 849.00 Length: 256
 Ratio: 4.082 Gaps: 3
 Percent Similarity: 81.250 Percent Identity: 64.844
 alignment_block:
 us-08-487-283a-8 x AA91026 ..
 Align seg 1/1 to: AA91026 from: 1 to: 436
 7 GATATCCAGATGACCCAGTCCCGTCCCTGCTGCGCTGGGCGA 56
 21 AspIleGlnMetAsnGlnSerProSerSerLeuSerAlaSerLeuGlyAs 37
 57 TAGGGTCAACATCACCCTGGCGCCGAGCAAAACATGTATGGCGCGCTGA 106
 37 pThrIleThrIleThrCysHisAlaSerGlnAsnIleAspValTyrLeuS 54
 107 ACTGTATGACGTAACCTGGGAAAGCTCCGAACTGTGATTTACGT 156
 54 erTyrTyrGlnGlnLysProGlyAsnValProLysLeuLeuIleTyrLys 70
 157 GCGAGAACCTGGCAGATGAGTCCCTGCTGCTGCTGATCCGCGTC 206
 71 AlaSerAsnLeuHisThrGlyValProSerArgPheSerGlySerGlySe 87
 207 CGGAACGATTTTCACCTGACCATGACGATGCTGACGCTGAAAGACTTCG 256
 87 rGlyThrGlyPheThrLeuThrIleSerSerLeuGlnProGlyAspIleA 104
 257 CTACGTATTACTGTGACGAACGTTTAAATACCTCCGTGACTTTCGACAG 306
 104 laThrTyTyrcysgnglnglnglnserTytyrProargThrPheGlygly 120
 307 GGTACCAGGTGGAATAAAGTACT..... 333
 121 GlnThrLysLeuGlnIleLysArgAlaAspAlaAlaProThrValSerle 137
 334GCGGTGGTGGTGTGCTGCGGATCTGCTGCGGCTTC 379
 137 uGlnGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGlySerG 154
 380 AAGTCCAACTGGTGCATCCGCGCGGAGTCAAGAACCGAGGCGCTCA 429
 154 luValGlnleuGlnInserGlyThrValLeuAlaArgProGlyAlaSer 170
 430 GTCAAGTGTCTGTAAAGTACGCGGTATATTTTCTTAATTATTTGAT 479
 171 ValLysMetSerCysLysAlaSerGlyTyThrPheAsnSerTytyrPhe 187
 480 TCAATGGGTGCTGACGCGCGCGGAGGCTGCAATGAGTGGTGAA 529
 187 HisTyrValLysGlnArgProGlyGlnGlyLeuGlnutprileglyle 204
 530 TCTTACCGGCTCTGTAGACACCAATATACGAAATTTTAAAGACCT 579
 204 IeTytyrProGlyAsnSerAspIleSerTytyrSerGlnAsnPheLysAspArg 220
 580 GTTACTAGACCGCTGACACTTGCATGTAGTACAGTATACATGAGCTTC 629
 221 AlaLysLeuThrAlaValThrSerThrAlaTyMetGlnleuThr 237
 630 CAGCTGCGATCGAGACACCGCGCTCTATTTATTCGCGCGT.....T 673
 237 gSerLeuThrAsnGlnAspSerAlaValTytyrPheCysThrLysGlnGly 254
 674 ATTTTGGTCTTACCGCAATGGTATTTTGGGTGCAAGCA 723

```

||  ::  ::  ::||| |||||
254 yAspTyrAspThr.....LeuAspTyrTrpGlyGlnGly 265
724 ACCCGTGCACGTGTCTG 741
||| ||||| |||
266 ThrSerValThrGlySer 271
seq_name: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:AAV43749

```

seq_documentation_block:

ID AAV43749 standard; Protein: 531 AA.

AAV43749;

11-FEB-2000 (first entry)

Amino acid sequence of the bscCD19xCD3 antibody.

bscCD19xCD3 antibody; bispecific single-chain fragment; CD19 antigen;
 CD3 antigen; CD19-positive target cell; T-cell stimulation;
 cytotoxic T-lymphocyte; B-cell malignancy; myasthenia gravis;
 B-cell mediated autoimmune disease; Morbus Basedow;
 Hashimoto thyroiditis; Goodpasture syndrome; B-cell depletion;
 non-Hodgkin lymphoma; gene therapy; cancer; viral disease.

Synthetic.

```

Key      Location/Qualifiers
FT       1..19      /note= "signal peptide"
FT       28..138   /note= "VL-CD19 peptide"
FT       154..277   /note= "VH-CD19 peptide"
FT       283..401   /note= "VH-CD3 peptide"
FT       420..525   /note= "VL-CD3 peptide"
FT       526..531   /note= "His tag"
FT       Peptide

```

W0954440-A1.

28-OCT-1999.

21-APR-1999; 99WO-EP02693.

21-APR-1998; 98EP-0107269.

(DOER/) DOERKEN B.

(RIET/) RIETHMUELLER G.

Kufer P, Lutterbuese R, Bargou R, Loeffler A;

WPI: 2000-013241/01.

N-PSDB; AAZ30332.

Novel multifunctional polypeptide for treating B-cell malignancies

especially non-Hodgkin lymphoma

Example 2; Fig 8; 91p; English.

The present sequence represents a bscCD19xCD3 antibody. This antibody is a bispecific single-chain polypeptide comprising domains providing binding-site of immunoglobulin chains or antibodies specifically recognizing CD19 and CD3 antigen. The polypeptide destroys CD19-positive target cells without any need of T-cell pre and/or co-stimulation, by recruiting cytotoxic T-lymphocytes and so specific lysis by T-cells rather than a direct effect by an antibody is achieved. The bispecific single-chain polypeptides, or nucleotides encoding them, are used for the treatment of B-cell malignancies, B-cell mediated autoimmune diseases like myasthenia gravis, Morbus Basedow, Hashimoto thyroiditis or Goodpasture syndrome or for the depletion of B- cells and more

CC particularly non-Hodgkin lymphoma in mammals preferably human. They can
 CC also delay the pathological conditions caused by these diseases, and
 CC can be used for detecting these diseases. The polynucleotide is used
 CC for gene therapy. The polypeptides are also used for identifying
 CC compounds modulating B-cell/T-cell mediated immune response with can
 CC turn be used for treating cancer, its related diseases and also for
 CC inhibiting viral diseases by preventing viral infection.

Sequence 531 AA:

alignment_scores: Length: 252
 Quality: 822.00
 Ratio: 3.914
 Gaps: 4
 Percent Similarity: 83.333 Percent Identity: 62.698

alignment_block:

US-08-487-283a-8 x AAV43749 ..

Align seg 1/1 to: AAV43749 from: 1 to: 531

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7  GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCGGCGGA 56
|||||.....|
28  AsplGlnLeuThrGlnSerProAlaSerLeuAlaValSerLeuGly 44
57  TAGGGTCACATCACCTGCGCGCGCGCAAAACATC...TATGGCGCG. 102
|||||.....|
44  nArAlaThrIleSerCysLysAlaSerClnSerValAspIyrAspGly 61
103  ....CTGACTGTATCAACCTGAACCTGGGAAGCTCCGACGCTT 144
|||||.....|
61  spSerTyrLeuAsnTrpTyrGlnGlnIleProGlyGlnProProLysLeu 77
145  CTGATTTACGGTCGCGACGACCTGGCAATGAGACCTTCCGCTTC 194
|||||.....|
78  LeuIleTyrAspAlaSerAsnLeuValSerIleProProAlaGlyPhe 94
195  TGGATCCGCGCTCCGGAACGATTCCTGACATCAGTCCAGTCCGAGC 244
|||||.....|
94  rGlySerClySerGlyThrAspPheThrLeuAsnIleHisProValGlu 111
245  CTGAAGACTTCGCTACGTATTACTGTCAGAACGTTTAAATACCTCGT 294
|||||.....|
111  ySValAspAlaIleThrTyrHisCysGlnIleSerThrGluAspProTyr 127
295  ACTTTCGACAGCGTACCAAGTGTGAATTAACCTACTGCGCGGTGG 344
|||||.....|
128  ThrPheGlyGlyGlyThrLysLeuGluIleLys....GlyGlyGly 142
345  TTCTGTCGCGGTGATCTGTGTGGCGGCTTCACATCCCAACTGGGTC 394
|||||.....|
142  ySerGlyGlyGlyGlySerGlyGlyGlySerClnValGlnLeuGln 159
395  AATCCGGCGCGGAGGTCAAGAACCGGCGCTCAGTCAAAAGTCTCTGT 444
|||||.....|
159  InSerGlyAlaGlnIleuValArgProGlySerSerValIylSerCys 175
445  AAACCTAGCGGCTATTTTCTAATATGATGATCAATGGGTCGCA 494
|||||.....|
176  LysAlaSerGlyTyrAlaPheSerSerTyrTrpMetAsnTrpValLys 192
495  GGCCCGCGCGGCGGCGTGAATGATGAGTGTACCTTACCGGCGCTCT 544
|||||.....|
192  nArgProGlyGlnGlyLeuGlnIleTrpIleGlyIleIleTrpProGlyAsp 209
545  GTACACCGAATATACCGAAATTTTAAAGACCGGTACTATGACGGCT 594
|||||.....|
209  LysAspTrpAsnTyrAsnGlyLysPheLysGlyLysAlaThrLeuThrAla 225
595  GACACTTCGACTACTACGATATACATGAGAGCTTCACGCTCGGATGCA 644
|||||.....|
226  AspluSerSerSerThrAlaTyrMetClnLeuSerSerLeuAlaSerG 242

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 07:47:39 ; Search time 10.02 Seconds

(without alignments)
71.793 Million cell updates/sec

Title: US-08-487-283A-1

Perfect score: 107

Sequence: 1 VIDHGTSSKCVROKVEGSS 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 segs, 34255486 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	24.3	21	1	OMP1_ACTPL
2	24	22.4	21	1	OMP1_HAEPK
3	23	21.5	14	1	RS19_PWPBP
4	22.5	21.0	20	1	LPTK_BACST
5	22	20.6	17	1	UN15_CLOPA
6	21	19.6	12	1	NO40_IOTJA
7	21	19.6	12	1	NO40_SSSRO
8	21	19.6	13	1	NO40_PFA
9	21	19.6	13	1	NO40_VICSA
10	21	19.6	14	1	SCR3_LEIQU
11	21	19.6	14	1	UN37_CLOPA
12	21	19.6	19	1	ALL7_OLEEU
13	21	19.6	21	1	MISC_MISAN
14	21	19.6	21	1	OMP4_PASHA
15	20	18.7	20	1	OSMB_SALTY
16	20	18.7	20	1	THAN_PODMA
17	19	17.8	13	1	CPI_APLCA
18	19	17.8	14	1	HCVL_MEGCR
19	19	17.8	17	1	MDH_ACIDE
20	19	17.8	17	1	PROP_SALTY
21	19	17.8	18	1	FIXA_RHILE
22	19	17.8	18	1	TKN2_SCYCA
23	19	17.8	18	1	TOP1_KLEAE
24	19	17.8	20	1	CUDP_VERCH
25	18	16.8	9	1	SAP_STOVA
26	18	16.8	10	1	COX4_THUOB
27	18	16.8	14	1	UN07_CLOPA
28	18	16.8	17	1	LPM_BRELA
29	18	16.8	17	1	PSBL_SYNVU
30	18	16.8	18	1	AZM_OCTVU
31	18	16.8	19	1	COXK_THUOB
32	18	16.8	19	1	LCRP_PETMA
33	18	16.8	20	1	OMPI_ACTAC

34	18	16.8	21	1	RT5_HAIME	P50557 halobacteri
35	17.5	16.4	20	1	FLA2_SPIAU	P21985 spirochaeta
36	17	15.9	10	1	AMPN_HELAM	P81731 heliocoverta
37	17	15.9	10	1	FARP_LOCOMI	P38553 locusta mig
38	17	15.9	10	1	GALU_HUMAN	P01358 homo sapien
39	17	15.9	10	1	LCMS_LEIMA	P21144 leucophaea
40	17	15.9	10	1	NEMS_DROME	P41494 drosophila
41	17	15.9	12	1	RS19_CLYEP	Q46490 clover yell
42	17	15.9	13	1	FLIBB_HYLLA	P14472 hylobates 1
43	17	15.9	13	1	TA13_TREME	P01370 tremella me
44	17	15.9	14	1	RS19_PRUAP	Q44160 prunus arme
45	17	15.9	15	1	LPL_THERM	P21234 thermus aqu

ALIGNMENTS

RESULT 1	OMP1_ACTPL	STANDARD;	PRT;	21 AA.
AC	P80368;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	40 KDA MAJOR OUTER MEMBRANE PROTEIN (MOMP) (FRAGMENT).			
OS	Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Actinobacillus.			
OC	NCBI_TaxID=715;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=598;			
RX	MEDLINE=96065432; PubMed=7483902;			
RA	Hartmann L., Schroeder W., Luebke-Becker A.;			
RT	"Isolation of the major outer-membrane protein of Actinobacillus			
RT	pleuropneumoniae and Haemophilus parasuis.";			
RL	J. Vet. Med. B 42:59-63(1995).			
CC	-1- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY			
CC	BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH			
CC	THE INTRACELLULAR RETICULATE BODY MEMBRANE.			
CC	-1- SUBUNIT: DISULFIDE BONDS INTERACTIONS WITHIN AND BETWEEN MOMP			
CC	MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.			
KW	Outer membrane; Transmembrane; Porin.			
FT	NON TER 21			
FT	SEQUENCE 21 AA; 2293 MW; FFE7D12EA916563B CRC64;			
Qy	1 VIDHGTSSKCVROKVEGS 20			
Db	3 VYDAEGTK-----VOIDGS 16			
Query Match	24.3%; Score 26; DB 1; Length 21;			
Best Local Similarity	35.0%; Pred. No. 3.4e+02;			
Matches	7; Conservative 4; Mismatches 3; Indels 6; Gaps 1;			
RESULT 2	OMP1_HAEPK	STANDARD;	PRT;	21 AA.
AC	P80369;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	MAJOR OUTER MEMBRANE PROTEIN (MOMP) (FRAGMENT).			
OS	Haemophilus parasuis.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Haemophilus.			
OC	NCBI_TaxID=738;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=A493;			
RX	MEDLINE=96065432; PubMed=7483902;			


```

DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DS UNKNOWN PROTEIN CP 15 FROM 2D-PAGE (FRAGMENT).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
CC Clostridium.
CX NCBI_TaxID=1501;
RN (1)
RP SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RL Electrophoresis 19:802-806(1998).
FT -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.1. ITS MW IS: 38.9 KDA.
SC NON_TER 17 17
SQ SEQUENCE 17 AA; 2015 MW; 46F8DBDC1A1CB4A CRC64;

Query Match 20.6%; Score 22; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 QKVEG 19
||:|
Db 4 QKLEG 8

RESULT 6
ID NO40_LOTJA STANDARD; PRT; 12 AA.
NO40_LOTJA
AC 022426;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EARLY NODULIN 40.
GN ENOD40.
OS Lotus japonicus.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Lotus.
CX NCBI_TaxID=34305;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV, GIFU;
RA Chian R.-J., Greshoff P.M.;
RT "Isolation and Primary Characterization of genomic Enod40 gene from
RL Lotus japonicus cultivar 'Gifu'."
CC (In) Plant Gene Register PGR97-142.
-1- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
SIMILIARITY)
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
DEVELOPMENT.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF013594; AAB82785.1; -.
KW Nodulation.
SQ SEQUENCE 12 AA; 1480 MW; 3C61E8257CB326C3 CRC64;

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OY      12 CWRKVEGS 20
      | : : |
Db      4 CWRKSHGS 12

RESULT 7
NO40_SESRO STANDARD: PRT: 12 AA.
AC      024369;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      EARLY NODULIN 40.
GN      ENOD40.
OS      Sesbania rostrata.
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC      Fabales; Fabaceae; Papilionoideae; Sesbania.
OX      NCBI_TaxID=3895;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Stem nodules;
RX      MEDLINE=98281575; PubMed=9620265;
RA      Corlich V., Goormachtig S., Lievekens S., van Montagu M., Holsters M.;
RT      "Patterns of ENOD40 gene expression in stem-borne nodules of Sesbania
      rostrata.";
RL      Plant Mol. Biol. 37:67-76(1998).
CC      -I- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
      GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
      STIMILARITY).
CC      -I- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
      DEVELOPMENT.
-----
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-----
DR      EMBL; Y12714; CAA73252.1; -.
KW      Nodulation.
SQ      SEQUENCE 12 AA; 1418 MW; 3C6955187CB326C3 CRC64;

Query Match 19.6%; Score 21; DB 1; Length 12;
Matches 3; Similarity 33.3%; Pred. No. 1.2e+03;
Match 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY      12 CWRKVEGS 20
      | : : |
Db      4 CWRKSHGS 12

RESULT 8
NO40_PEA STANDARD: PRT: 13 AA.
AC      P55953;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      EARLY NODULIN 40.
GN      ENOD40.
OS      Pisum sativum (Garden pea).
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC      Fabales; Fabaceae; Papilionoideae; Pisum.
OX      NCBI_TaxID=3888;
RN      [1]
RP      SEQUENCE FROM N.A.

```

RC STRAIN-CV. SPARKLE; TISSUE-Root nodules;
 RX MEDLINE=95036021; PubMed=7948896;
 RA Matvienko M., van de Sande K., Yang W.C., van Kammen A., Bisseling T.,
 RA Franssen H.J.;
 RT "Comparison of soybean and pea ENOD40 cDNA clones representing genes
 expressed during both early and late stages of nodule development.";
 RL Plant Mol. Biol. 26:487-493(1994).
 CC -1- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
 CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
 CC SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
 CC DEVELOPMENT.
 CC -----
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 CC -----
 CC EMBL: X81064; -; NOT_ANNOTATED_CDS.
 CC Nucleotide
 CC Modulation
 CC SEQUENCE 13 AA: 1565 MW; 3C695B66BD8A26C3 CRC64;
 SQ
 Query Match 19.6%; Score 21; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 12 CVROKVEGS 20
 | : : : |
 Db 5 CWOKSINGS 13
 RESULT 9
 NO40_VICSA STANDARD; PRT; 13 AA.
 ID NO40_VICSA P55961;
 AC P55961;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE EARLY NODULIN 40.
 GN ENOD40.
 OS Vicia sativa (Spring vetch) (Tare).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Vicia.
 OX NCBI_TaxID=3908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIGRA; TISSUE-Root nodules;
 RX MEDLINE=96011756; PubMed=7548828;
 RA Vijn I., Yang W.-C., Pallsgaard N., Oostergaard Jensen E.,
 RA van Kammen A., Bisseling T.;
 RT "VENOD5, VENOD12 and VENOD40 expression during Rhizobium-induced
 RT nodule formation on Vicia sativa roots.";
 RL Plant Mol. Biol. 28:1111-1119(1995).
 CC -1- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
 CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
 CC SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING RHIZOBIUM-INDUCED NODULE
 CC FORMATION. IN 4-DAY OLD NODULES IT IS FOUND IN ALL THE CELLS OF
 CC THE CENTRE OF THE NODULE PRIMORDIUM AND ALSO OCCURS IN THE REGION
 CC OF THE ROOT PERICYCLE FACING THE NODULE PRIMORDIUM. AT DAY 5,
 CC EXPRESSION IS SEEN IN THE COMPLETE CENTRAL TISSUE. AT DAY 20
 CC EXPRESSED IN THE COMPLETE PREFIXATION ZONE II, AND IN THE PROXIMAL
 CC PART OF THIS ZONE IT IS FOUND ONLY IN THE INFECTED CELLS BUT NOT
 CC IN THE UNINFECTED CELLS. AT THE TRANSITION OF PREFIXATION ZONE II
 CC INTO INTERZONE II-III EXPRESSION DECREASES IN THE INFECTED CELLS.
 CC IN THE FIXATION ZONE III, EXPRESSION IS INDUCED IN THE UNINFECTED
 CC CELLS AND IN THE PROXIMAL PART OF THIS ZONE IT IS UNDETECTABLE.
 CC PRESENT AT HIGH LEVELS IN THE PERICYCLE OF THE NODULE VASCULAR

CC BUNDLE.
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 CC -----
 CC EMBL: X83683; -; NOT_ANNOTATED_CDS.
 CC Nucleotide
 CC Modulation
 CC SEQUENCE 13 AA: 1531 MW; 3C6953C4BD8A26C3 CRC64;
 SQ
 Query Match 19.6%; Score 21; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 12 CVROKVEGS 20
 | : : : |
 Db 5 CWOKSINGS 13
 RESULT 10
 SCK3_LEIOU STANDARD; PRT; 14 AA.
 ID SCK3_LEIOU P45661;
 AC P45661;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE LEIURTOXIN III (FRAGMENT).
 OS Leiurus quinquestratus quinquestratus (Egyptian scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butiidae; Butiidae; Leiurus.
 OX NCBI_TaxID=6885;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=93075256; PubMed=1280139;
 RA Valdivia H.H., Martin B.M., Escobar L., Possani L.D.;
 RA "Noxiustoxin and leiurotoxin III, two homologous peptide toxins with
 RT binding properties to synaptic membrane K⁺ channels.";
 RL Biochem. Int. 27:953-962(1992).
 CC -1- FUNCTION: BLOCKER OF POTASSIUM CHANNELS.
 CC -1- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
 CC CHANNEL INHIBITORS SUBFAMILY.
 CC InterPro: IPR001947;
 DR PROSITE: PS01138; SCORP_SHORT_TOXIN; PARTIAL.
 KM Neurotoxin; Potassium channel inhibitor.
 FT NON_TER 14
 SQ SEQUENCE 14 AA: 1588 MW; 83C67CCBD691205E CRC64;
 Query Match 19.6%; Score 21; DB 1; Length 14;
 Best Local Similarity 41.7%; Pred. No. 1.4e+03;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VIDHOGTKSSKC 12
 | : : : |
 Db 2 LIDVRCYDSSQC 13
 RESULT 11
 UN37_CLOPA STANDARD; PRT; 14 AA.
 ID UN37_CLOPA P81358;
 AC P81358;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE UNKNOWN PROTEIN CP 37 FROM 2D-PAGE (FRAGMENT).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;

```

OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=M5;
RA MEDLINE=98291870; PubMed=9629918;
RT Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.8, ITS MW IS: 44.7 KDA.
FT NON_TER 14
SO SEQUENCE 14 AA; 1579 MW; 0538462DEF89210 CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 14;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 IDHOGTK 8
Db 7 IEDQGVK 13

RESULT 12
ALIT_OLIEU
ID ALL7_OLIEU STANDARD; PRT; 19 AA.
AC P81430;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE POLLEN ALLERGEN OLE E 7 (OLE E VII) (FRAGMENT).
OS Olea europaea (Common olive).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Lamiales; Oleaceae; Olea.
OX NCBI_TaxID=4146;
RN [1]
RP SEQUENCE.
RC TISSUE=Pollen;
RA Tejera M.L., Villalba M., Rodriguez R.;
RT "Isolation and characterization of Ole e 7, a new allergen from olive
RT tree pollen.";
RL Submitted (JUL-1998) to the SWISS-PROT data bank.
KW Allergen.
FT NON_TER 19
SO SEQUENCE 19 AA; 1986 MW; 999A5008C41A67E CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 19;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 OGFKSK 11
Db 4 OCTVTAK 10

RESULT 13
MISG_MISAN
ID MISG_MISAN STANDARD; PRT; 21 AA.
AC P81474;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MISGURIN.
OS Misgurnus anguillicaudatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cobitidae; Misgurnus.
OX NCBI_TaxID=75329;
RN [1]

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RP SEQUENCE.
RX MEDLINE=97415401; PubMed=9271200;
RA Park C.B., Lee H.J., Park I.Y., Kim M.S., Kim S.C.;
RT "A novel antimicrobial peptide from the loach, Misgurnus
RT anguillicaudatus.";
RL FBS Lett. 411:173-178(1997).
CC -1- FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST SEVERAL
CC -1- GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA AND FUNGI.
CC -1- MASS SPECTROMETRY: MW=2502; METHOD=MALDI.
KW Antibiotic; Fungicide.
SO SEQUENCE 21 AA; 2502 MW; 4A6E9D0AB391BCF1 CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 14 RORVE 18
Db 1 RORVE 5

RESULT 14
OMPA_PASHA
ID OMP4_PASHA STANDARD; PRT; 21 AA.
AC P80228;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MAJOR OUTER MEMBRANE PROTEIN P44 (OMP) (FRAGMENT).
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE.
RC STRAIN=BIOVAR A / SEROVAR 1 129;
RX MEDLINE=95102227; PubMed=7803929;
RA Luebke A., Hartmann L., Schroeder W., Hellmann E.;
RT "Isolation and partial characterization of the major protein of the
RT outer membrane of Pasteurella haemolytica and Pasteurella
RT multocida.";
RL Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 281:45-54(1994).
CC -1- SUBUNIT: MONOMER (PROBABLE).
KW Outer membrane; Porin.
FT NON_TER 21
SO SEQUENCE 21 AA; 2286 MW; E6EF82BEACT7BB63B CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 21;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 VIDHGTK 8
Db 3 YDAEGSK 10

RESULT 15
OSMB_SALTY
ID OSMB_SALTY STANDARD; PRT; 20 AA.
AC P37723;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OSMOTICALLY INDUCIBLE LIPOPROTEIN B (FRAGMENT).
OS OSMB.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
SO SEQUENCE FROM N.A.

```

RX MEDLINE=87190435; PubMed=2436909;
 RA Theisen M., Keilin R.A., Neuhard J.;
 RT "Cloning and characterization of the pyrF operon of Salmonella
 RT typhimurium.";
 RL Eur. J. Biochem. 164:613-619(1987).
 RN [2]
 RP IDENTIFICATION.
 RX MEDLINE=95004589; PubMed=7920643;
 RA Robison K., Gilbert W., Church G.M.;
 RT "Large scale bacterial gene discovery by similarity search.";
 RL Nat. Genet. 7:205-214(1994).
 CC -1- FUNCTION: PROVIDES RESISTANCE TO OSMOTIC STRESS. MAY BE IMPORTANT
 CC FOR STATIONARY-PHASE SURVIVAL.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
 CC ANCHOR (PROBABLE).
 CC -1- INDUCTION: BY ELEVATED OSMOTIC PRESSURE IN THE GROWTH MEDIUM.
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 CC -----
 CC EMBL: X05382; -; NOT_ANNOTATED_CDS.
 DR STyGene; SG10272; OSMB.
 DR InterPro: IPR000437; -;
 DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; PARTIAL.
 KW Membrane; Lipoprotein.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 1792 MW; FCCID85EC27ABC87 CRC64;

Query Match 18.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. NO. 3e+03; 1; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 1; Indels 0;

QY 1 VIDHO 5
 || ||
 Db 13 VIGHQ 17

Search completed: July 19, 2001, 07:50:21
 Job time: 162 sec

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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:46:49 ; Search time 12.72 Seconds

(without alignments)
125.760 Million cell updates/sec

Title: US-08-487-283A-1

Perfect score: 107

Sequence: 1 VIDHGTGSKSKCYRQKVEGSS 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4046

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	28.0	16	2	PH1589
2	25	23.4	15	2	PH1582
3	25	23.4	18	2	S45373
4	23	23.4	19	2	S02808
5	23	21.5	12	2	PH1675
6	23	21.5	13	2	PH1676
7	23	21.5	14	2	PH1677
8	23	21.5	15	2	I67525
9	23	21.5	16	2	D45193
10	23	21.5	17	2	B86323
11	23	21.5	18	2	PH1621
12	23	21.5	19	2	T50329
13	23	21.5	20	2	A44927
14	23	21.5	20	2	S19618
15	23	21.5	21	2	PH1688
16	22.5	21.0	20	1	LFBS7U
17	22.5	21.0	20	1	S23742
18	22	20.6	11	2	A33917
19	22	20.6	14	2	S11074
20	22	20.6	14	2	PH1311
21	22	20.6	15	2	PH0753
22	22	20.6	16	2	F57789
23	22	20.6	16	2	JQ2306
24	22	20.6	16	2	JQ2316
25	22	20.6	16	2	I51879
26	21	19.6	13	2	S60046
27	21	19.6	13	2	S52356
28	21	19.6	13	2	S23638
29	21	19.6	14	2	A48389

30	21	19.6	14	2	S23639	Ig kappa chain J s
31	21	19.6	15	2	PH1320	Ig heavy chain DJ
32	21	19.6	16	2	S28433	major outer membra
33	21	19.6	17	2	S48655	glutathione dehydr
34	21	19.6	17	2	I57941	beta 3-adrenergic
35	21	19.6	20	2	C44907	manganese peroxida
36	21	19.6	21	2	S03506	T-cell receptor al
37	20	18.7	9	4	I73804	hypothetical E2 pr
38	20	18.7	13	2	A26999	carboxylesterase (
39	20	18.7	14	2	C44823	synaptosomal-assoc
40	20	18.7	15	2	F29501	fibrinopeptide A -
41	20	18.7	15	2	PA0036	glycine cleavage s
42	20	18.7	16	2	A49226	major outer membra
43	20	18.7	16	2	B48406	annexin VI homolog
44	20	18.7	17	2	I49425	mitogen regulated
45	20	18.7	17	2	C37396	pollen allergen Fe

ALIGNMENTS

RESULT 1
PH1589
Ig H chain V-D-J region (wild-type clone 140) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1589
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A/Reference number: PH1580; MUID:93301609
A/Accession: PH1589
A/Molecule type: DNA
A/Residues: 1-16 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: Immunoglobulin

Query Match 28.0%; Score 30; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 CVRQKVEGS 20
DB 1 CARQSYDGS 9

RESULT 2
PH1582
Ig H chain V-D-J region (wild-type clone 5) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A/Reference number: PH1580; MUID:93301609
A/Accession: PH1582
A/Molecule type: DNA
A/Residues: 1-15 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 23.4%; Score 25; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 CVRQKVEGS 20
DB 1 CARQSYDGS 9

RESULT 3
S45373
translation elongation factor EF-1a - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C:Accession: S45373
R:Marly, I.; Brugidou, C.; Chartier, Y.; Meyer, Y.
Plant J. 4, 265-278, 1993
A:Title: Growth-related gene expression in Nicotiana tabacum mesophyll protoplasts.
A:Reference number: S45372; MUID:94035181
A:Accession: S45373
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <MA>
A:Cross-references: EMBL:Z14080; NID:9443955; PIDN:CAA78458.1; PID:9443956

Query Match 23.4%; Score 25; DB 2; Length 18;
Best Local Similarity 35.7%; Pred. No. 1.3e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 DHGKSSKCYROR 16
DB 3 DPTGAKYTKAQAOK 16

RESULT 4
S02808
nucleolin - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S02808
R:Sapp, M.; Richer, A.; Weissbart, K.; Calzergues-Ferrer, M.; Amalric, F.; Wallace, M.C.
Eur. J. Biochem. 179, 541-548, 1989
A:Title: Characterization of a 48-kDa nucleic-acid-binding fragment of nucleolin.
A:Reference number: S02808; MUID:9153087
A:Accession: S02808
A:Molecule type: protein
A:Residues: 1-19 <SAP>

Query Match 23.4%; Score 25; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 QKVEG 19
DB 15 QKVEG 19

RESULT 5
PH1675
Ig heavy chain V region (clone NP-6-7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1675
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607
A:Accession: PH1675
A:Molecule type: mRNA
A:Residues: 1-12 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 21.5%; Score 23; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 5 QGTRSSK 11

DB 6 RGTSTRE 12

RESULT 6
PH1676
Ig heavy chain V region (clone NP-6-5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1676
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607
A:Accession: PH1676
A:Molecule type: mRNA
A:Residues: 1-13 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 21.5%; Score 23; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 5 QGTRSSK 11
DB 6 RGTSTRE 12

RESULT 7
PH1677
Ig heavy chain V region (clone NP-6-6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1677
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607
A:Accession: PH1677
A:Molecule type: mRNA
A:Residues: 1-14 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 21.5%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 5 QGTRSSK 11
DB 6 RGTSTRE 12

RESULT 8
167525
CD3 antigen homolog - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998
C:Accession: 167525
R:Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice
A:Reference number: 153392; MUID:94298870
A:Accession: 167525
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <RES>
A:Cross-references: GB:S71349; NID:9550037

C:Genetics:
A:Gene: Ig VH7183

Query Match 21.5%; Score 23; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 12 CVRQKVGSS 21
| | | | |
Db 2 CARRDHGSS 11

RESULT 9
D45193
zinc finger protein ZNF60 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 01-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: D45193
R:Lichter, P.; Bray, P.; Ried, T.; David, I.B.; Ward, D.C.
Genomics 13, 999-1007, 1992
A:Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile sites
A:Reference number: A43284; MUID:92372070
A:Accession: D45193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <LIG>
A:Cross-references: GB:M88369; NID:9340475; PIDN:AAA61327.1; PID:9340476
A:Note: sequence extracted from NCBI backbone (NCBIN:111662, NCBIPI:111664)

Query Match 21.5%; Score 23; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 HOGTKSSKC 12
| | | | |
Db 2 HTGKPFSC 10

RESULT 10
B86323
protein F14D16.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B86323
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huiztar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: B86323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <STO>
A:Cross-references: GB:AE05172; NID:98778270; PIDN:AAF79279.1; GSPDB:GN00141
C:Genetics:
A:Gene: F14D16.5
A:Map position: 1

Query Match 21.5%; Score 23; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 HOGTKSSKC 12
| | | | |

Db 8 HHLSPSSRC 16

RESULT 11
PH1621
Ig H chain V-D-J region (clone B-less 41) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1621
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m J. Exp. Med. 178, 317-329, 1993
A:Reference number: PH1580; MUID:93301609
A:Accession: PH1621
A:Molecule type: DNA
A:Residues: 1-18 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 21.5%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 CVRQ 15
| | | | |
Db 1 CVRQ 4

RESULT 12
T50329
wd-repeat protein popl. [imported] - fission yeast (Schizosaccharomyces pombe) (fragm
C:Species: Schizosaccharomyces pombe
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50329
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25062
A:Accession: T50329
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <LYN>
A:Cross-references: EMBL:AL157874; PIDN:CA875991.1; GSPDB:GN00067; SPDB:SPBC1718.01
A:Experimental source: strain 972h(-); cosmid c1718
C:Genetics:
A:Gene: SPBC262.18; SPDB:SPBC1718.01
A:Map position: 2

Query Match 21.5%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VIDHGTSS 10
| | | | |
Db 10 VLEFGSTKSS 19

RESULT 13
A44927
major outer membrane protein 28k chain - Legionella pneumophila (fragment)
N:Alternate names: major outer membrane protein 31k chain
C:Species: Legionella pneumophila
C>Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Mar-1996
C:Accession: A44927; B44927
R:Hoffman, P.S.; Seyer, J.H.; Butler, C.A.
J. Bacteriol. 174, 908-913, 1992
A:Title: Molecular characterization of the 28- and 31-kilodalton subunits of the LegI
A:Reference number: A44927; MUID:921211130
A:Accession: A44927
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <HOF>

A: Experimental source: SVIR Philadelphia 1, serogroup 1
 A: Note: sequence extracted from NCBI backbone (NCBIP:77834)
 A: Accession: B44927
 A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 4-17 <HO2>
 A: Experimental source: SVIR Philadelphia 1, serogroup 1
 A: Note: sequence extracted from NCBI backbone (NCBIP:77837)

Query Match 21.5%; Score 23; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 IDHOGT 7
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 Db 14 VPHEGT 19

RESULT 14

S19618
 globin - polychaete (Eudistylia vancouveri) (fragment)
 N: Alternate names: chlorocortin
 C: Species: Eudistylia vancouveri
 C: Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
 C: Accession: S19618
 R: Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.H.
 J. Mol. Biol. 222, 1109-1129, 1991
 A: Title: Hierarchy of globin complexes. The quaternary structure of the extracellular chain
 A: Reference number: S19532; MUID: 92106333
 A: Accession: S19618
 A: Molecule type: protein
 A: Residues: 1-20 <QAB>
 A: Experimental source: plume
 C: complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dodeca
 C: keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 21.5%; Score 23; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 IDHOGTKSSK 11
 : || | | |
 Db 10 IDANGKKGDK 19

RESULT 15

PH1688
 Ig heavy chain V region (clone NP-7-1) - mouse (fragment)
 C: Species: Mus musculus (house mouse)
 C: Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
 C: Accession: PH1688
 R: McHeyzer-Williams, M.G.; McLean, M.J.; Lajor, P.A.; Nossal, G.J.V.
 J. Exp. Med. 178, 295-307, 1993
 A: Title: Antigen-driven B cell differentiation in vivo.
 A: Reference number: PH1675; MUID: 93301607
 A: Accession: PH1688
 A: Molecule type: mRNA
 A: Residues: 1-21 <MCH>
 A: Experimental source: B cell
 C: Superfamily: immunoglobulin V region; immunoglobulin homology
 C: Keywords: heterotetramer; immunoglobulin

Query Match 21.5%; Score 23; DB 2; Length 21;
 Best Local Similarity 57.1%; Pred. No. 3.2e+03;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 5 OGTKSSK 11
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 Db 6 RGTKSTY 12

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17 pargValThrIleThrCysArgAlaSerGlnAspIleAsnSerTyrLeu 34
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207 CGGAACGATTTCTACTCTGACATCAGACATGACAGCTGACAGACTTCG 256
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257 CTACGATTTACTGTCAGAACGTTTAAATACCTCCGTTGACTTCGACAG 306
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: Sequence 147, Application US/08477484B
: Patent No. 5756599
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: APPLICANT: Carroll, Stephen F.
: APPLICANT: Studnika, Gary M.
: TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

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: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 169
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McAndrews, Held & Malloy, Ltd.
: STREET: 500 West Madison Street, 34th floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60661
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,484B
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/425,336
: FILING DATE: 18-APR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/064,691
: FILING DATE: 12-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/988,430
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/901,707
: FILING DATE: 19-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/787,567
: FILING DATE: 04-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: McNicholas, Janet M.
: REGISTRATION NUMBER: 32,918
: REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/707-8889
: TELEFAX: 312/707-9155
: TELEX: 650 388-1248
: INFORMATION FOR SEQ ID NO: 147:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 240 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-477-484B-147

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107 ACTGATATACGTAACCTGGAAAGCTCCGAAGCTTCTGATTTACGCT 156
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seq_documentation_block:
; Sequence 147, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567

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; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 32,918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-9155
; TELEFAX: 312/707-8889
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-839-765-147

alignment_scores:
Quality: 858.00 Length: 246
Ratio: 4.105 Gaps: 2
Percent Similarity: 84.959 Percent Identity: 66.667

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157 GCGAGAACCTGGCAGATGAGATCCCTTCTGCTGTGATCCGGCTC 206
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51 AlaAsnArgLeuGlnSerGlyValProSerArgPheSerGlySerGly 67
207 CGGAACGATTTCACTGACCATCAGCAGTGTGAGCGCTGGAAGCTTC 256
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67 rGlyThrAspTyrThrLeuThrIleSerSerLeuGlnIlyArgIle 84
257 CTACGTATTAATTCAGACGTTTAAATCTCCGTGACTTCGACAG 306
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307 GGTACCAAGGTGGAATTAACGTACTGCGCGGTGTGTTGTTGCGG 356
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101 GlyThrIlySerLeuGlnMetLys.....GlyGlyGlySerGlyGly 115
357 TGGATCTGGTGTGGCGGTGTCTCAAGTCACTGATGGAATCGCGGCG 406
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115 yglserglylglyglysergluileglnleuvalglnserglylg 132
407 AGGTACAGAACCGAGGGCGCTCAGTCAAGTGTCTGTAAGCTAGCGC 456
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557 ATACGAAATTTTAAAGACCGTGTACTATGACCGCTGACACTTGCACT 606

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215 LtyrPheCysThrArgArgGlyTyr.....AspTyrPhePhe 228
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seq_documentation_block:
; Sequence 147, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
; US-09-136-389-147

alignment_scores:
  Quality: 858.00      Length: 246
  Ratio: 4.105         Gaps: 2
  Percent Similarity: 84.959   Percent Identity: 66.667

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57 TAGGGTCACCATCACTCGCGCGCGCGAAGAAACATCTATGGCGGCTCA 106
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17 parGValThrIleThrCysArgAlaSerGlnAspIleAsnSerTyrLeu 34
107 ACTGATATCAAGTAAACCTGGGAAAGCTCCGAGCTGTGATTACGGT 156
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34 eTrpPheGlnGlnIleProGlyLysAlaProLysThrLeuIleTyrArg 50
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51 AlaAsnArgLeuGlnIleSerGlyValProSerArgPheSerGlySer 67
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67 rGlyThrAspTyrThrLeuThrIleSerSerLeuGlnTyrGluAspPhe 84
257 CTACGATATCACTGTCAGAACGTTTAAATACCTCCGTGACGACAG 306
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84 LylIeTyrTyrCysGlnGlnIleTyrAspIleSerProThrPheGly 100
307 GGTACCAAGGTGGAATAAAGCTACTGCGCGGTGTGTCTGTGGTGGCG 356
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101 GlnThrLysLeuGlnMetLys.....GlyGlyGlySerGlyGly 115
357 TGGATCTGGTGGTGGCGGTTCACAGTCACTGGTGCATCGGCGCGCG 406
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507 GGGCTGGAATGATGGTGAAGTCTTAACCGGCTGTGATGACCGCAAT 556
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607 AGTACGTATACATGAGCTCTCCAGCTCGATCGAGAGACGACGCCGT 656
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seq_name: /cgn2_6/ptodata/2/1aa/5a_COMB.pep:US-08-400-115-4
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; Sequence 41, Application US/08400115
; Patent No. 5864019
; GENERAL INFORMATION:
; APPLICANT: KING, David John
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; APPLICANT: YARRANTON, Geoffrey Thomas
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,115
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,136
; FILING DATE: 27-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,193
; FILING DATE: 17-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/00935
; FILING DATE: 11-JUN-1991
; APPLICATION NUMBER: GB 9012995.8
; FILING DATE: 11-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 040283/0106 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-400-115-4

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Quality: 857.50 Length: 247
Ratio: 4.123 Gaps: 2
Percent Similarity: 84.211 Percent Identity: 66.397

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454 GCGTATATTTTCTAATTAATGATTCATGAGTGGCTGACAGCCCGCG 503
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seq_name: /cgn2_6/ptodata/2/1aa/5a_COMB.pep:US-08-875-811-41
seq_documentation_block:
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

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MOLECULE TYPE: protein
US-08-875-811-49

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Quality: 795.50 Length: 246
Ratio: 3.938 Gaps: 2
Percent Similarity: 82.114 Percent Identity: 62.195

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Align seg 1/1 to: US-08-875-811-49 from: 1 to: 355

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; Sequence 64, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Luis
; APPLICANT: Kiodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fatis, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..355
; OTHER INFORMATION: /note="E6FB[Met-(-1)]SerIone"
US-08-875-811-64

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Quality: 795.50 Length: 246
Ratio: 3.938 Gaps: 2
Percent Similarity: 82.114 Percent Identity: 62.195

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US-08-487-283a-8 x US-08-875-811-64 ..

Align seg 1/1 to: US-08-875-811-64 from: 1 to: 355

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seq_documentation_block:
: Sequence 45, Application US/08875811
: Patent No. 6045793
: GENERAL INFORMATION:
: APPLICANT: Rybak, Susanna M.
: APPLICANT: Newton, Dianne L.
: APPLICANT: Boque, Luis
: APPLICANT: Mlodawer, Alexander
: TITLE OF INVENTION: Recombinant Ribonuclease Proteins
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-45

alignment_scores:
Quality: 795.50 Length: 246
Ratio: 3.938 Gaps: 2
Percent Similarity: 82.114 Percent Identity: 62.195

alignment_block:
US-08-487-283a-8 x US-08-875-811-45 ..
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57 TAGGTCACCATCAGCTGCGCGCGCAGCAAGCAATCATGATGACGCTGA 106
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APPLICATION NUMBER: US/08/875, 811
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/011, 800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-43

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alignment_scores:
Quality: 795.50      Length: 246
Ratio: 3.938        Gaps: 2
Percent Similarity: 82.114    Percent Identity: 62.193

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alignment_block:
US-08-487-283a-8 x US-08-875-811-43 ..

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seq_documentation_block:
; Sequence 18, Application US/08121054C
; Patent No. 5637481
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; TITLE OF INVENTION: Expression Vectors Encoding Bispecific
; TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,054C
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/013,420
; FILING DATE: 01-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.18US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-121-054C-18

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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C 17	459.6	61.3	762	10	I69485	I69485 Sequence 57
C 18	459.6	61.3	762	10	I73104	I73104 Sequence 57
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C 20	459.6	61.3	762	10	I87063	I87063 Sequence 57
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C 22	453.8	60.5	2178	9	AR054190	AR054190 Sequence
C 23	447.2	59.6	671	88	AF0531100	AF0531100 Homo sapi
C 24	443.2	59.1	687	9	AR105449	AR105449 Sequence
C 25	443.2	59.1	687	10	I65402	I65402 Sequence 1
C 26	442.2	59.0	6557	10	I26929	I26929 Sequence 3
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C 29	432.8	57.7	756	10	I69461	I69461 Sequence 29
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C 33	432.4	57.7	1673	93	HS16G11H	Y14737 Homo sapien
C 34	431.6	57.5	1404	9	A99058	A99058 Sequence 66
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C 41	417.6	55.7	664	85	AB027435	AB027435 Homo sapi
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C 44	415.8	55.4	1437	9	AR108865	AR108865 Sequence
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VERSION	AX076856			
KEYWORDS	AX076856.1	GI:13160364		
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ORGANISM	synthetic construct.			
REFERENCE	synthetic construct			
AUTHORS	artificial sequence.			
TITLE	1 (bases 1 to 1418)			
JOURNAL	Knick,V.C., Stimmel,J.B. and Thurmond,L.M.			
FEATURES	Combination of an anti-ep-cam antibody with a chemotherapeutic agent			
source	Patent: WO 0107082-A 4 01-FEB-2001;			
	GLAXO GROUP LIMITED (GB)			
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Matches 593; Conservative	0; Mismatches 137; Indels 18; Gaps 1;			
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OY	61 GTCCAAAGTGTGCATCCGGCGCGGAGGTCGAAGAGCCAGGGGCGCTCATGCAAAAGTGC 120 			
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OY	241 GAAATATTTAAAGACCGTGTCTATATGACGCGGTGACACTTGCATAGTACATATATACATG 300 			
DB	264 GAAATATTTCAAGGAGACGGTTTGCATTTCTCTAGACAAATCCGCCACACACCGCTATATG 323 			
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DB	666 ACCTCATCTGCAACGTAATTCACAAGGCCACAGCAACACCAAGGTGTGACAAAGATTGAG 725 			
OY	721 CCCAATCTTGTGACAAACTCACCAT 748 			
DB	726 CCCAATCTTGTGACAAACTCACCAT 753 			
RESULT 2				
HOMIGHEPAH				
LOCUS	HOMIGHEPAH 1599 bp mRNA			
DEFINITION	Human (hybridoma H210) anti-hepatitis A IgG variable region, constant region, complementarity determining regions mRNA, complete cds.			
ACCESSION	M87789			
VERSION	M87789.1 GI:185361			

KEYWORDS	complementarity-determining region; constant region; immunoglobulin gamma chain; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens CDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1599)
AUTHORS	Lewis,A.P., Lemon,S.M., Barber,K.A., Murphy,P., Parry,N.R., Peakman,T.C., Sims,M.J., Worden,J. and Crowe,J.S.
TITLE	Rescue, expression, and analysis of a neutralizing human anti-hepatitis A virus monoclonal antibody
JOURNAL	J. Immunol. 151 (5), 2829-2838 (1993)
MEDLINE	93367243
FEATURES	Location/Qualifiers
source	1..1599
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	1..34
sig_peptide	/note="putative"
	35..91
CDS	/note="putative"
	35..1465
	/note="Anti-hepatitis A; putative"
	/codon_start=1
	/product="IgG"
	/protein_id="AA02914.1"
	/db_xref="GI:185362"
	/translation="MDWTFLEFVVAATGVQSOMQVSGAEYKPKGSSVTYSCKAS
	GGTFNSAIISWROAPGSGLEMMGGITPLEGTPTYSNFGQVYITADKSTSAHML
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	SSISGDTALGCLVYKDYPRPPTVSNAGCALISGHTFPAYVLIQSSGLTSLSSVYTP
	KDTLMISRTPEPTCVVVDVSHDEPEVFNMYVDGVEVHNAKTKRREQVNSTYKRVSV
	LTVLHQMNLGKEKCKSNKALPAPIEKTISAKGQPREPQVYTLPPSRDELTKNQV
	SLTCLVPGSPSDIAVEESNGQPENNYKTPPYLDSGSEFLYSLTVDKSRMQGN
	VESGVNHEALHNHYTQKSLSLSPGK"
	92..472
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	/product="IgG"
gene	182..196
	/gene="CDR1"
misc_feature	182..196
gene	/gene="CDR1"
	/note="complementarity-determining region 1; putative"
	239..289
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gene	/gene="CDR2"
	/note="complementarity-determining region 2; putative"
	386..439
misc_feature	/gene="CDR3"
	/note="complementarity-determining region 3; putative"
gene	/gene="CDR3"
	473..1462
mat_peptide	/note="constant region; putative"
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3'UTR	/note="putative"
	1566..1571
polyA_signal	/note="putative"
BASE COUNT	357 a 526 c 441 g 275 t
ORIGIN	
Query Match	63.88; Score 478.2; DB 97; Length 1599;
Best Local Similarity	78.08; Pred. No. 3.5e-103;
Matches 595; Conservative	0; Mismatches 153; Indels 15; Gaps 1;
1	ATGAAGTGAGACTGGGTATTCCTCTCTCCGTACGTACTGCCGCGGTCCAGTCCCA 60
35	ATGAGCTGGAGCTGGAGTTCCTCTTTGTGGTGGAGCAGGTACAGAGTGTCAAGTCCAG 94
61	GTCACATGTGTCAATCCGCGCGCGAGGTCAAGAACCGAGGGGCGCTAGTCAAAAGTTC 120

Query Match	63.5%	Score 476	DB 9	Length 9209
Db	95	ATGCAAGTGGTCACTCTGGGCTGAAGTAAAGAAAGCTGGGCTCTCGGTACGGTCTCC	154	
Qy	121	TGTAAAGTCAGCGGGTATATTTTCTTAATATATGGAATTCATGGGTGGTCAGGCCCC	180	
Db	155	TCCAAAGGCACTGAGAGGCAACCTTCAGCAACATGCTATCAGTGGGTGGAGACGGCCCT	214	
Qy	181	GGGCAAGGCGCTGGAAATGATGGGTGAGATCTTACCGGGCTCTGTGAGCAGCAATATACC	240	
Db	215	GGACAAAGGCTTGAATGGTGGAGGAGATCATCCCTCTTTTGGTACACCAACCTACATCA	274	
Qy	241	GAAATTTTAAAGACCGTGTACTATGACCGCTGACACTGTACATGATACATATACATG	300	
Db	275	CGAACCTTCACAGGAGAGATCAGATTCACCGCGCAAAATCCACAGCACAGCCCAATG	334	
Qy	301	GAGCTCTCCAGCGCTCGATCGAGAGACACGGCGCTCTATTTATGGCGCGTTAT-----	354	
Db	335	GAGCTGATCAGCGCTGAGATCTGAGGACACAGGCGCGTGTATCTGTGCGCAGATGGCTAC	394	
Qy	355	-----TTTTTGGTTCTAGCCCGAAATGGTATATTTGATGTTTGGGGTCAAGAAAC	405	
Db	395	AGGCAAGCAATTTTATGACCGGGGCCGGGTGGCTGTGTGACCCCTCGGGGCGAGGGCAC	454	
Qy	406	CTGGTCACTGTCTCGAGGCGCTTCACACAAAGGCGCCATGGTCTTCCCTTGGCGGCCACC	465	
Db	455	CTGGTCACTGTCTCGAGGCGCTTCACACAAAGGCGCCATGGTCTTCCCTTGGCGGCCACC	514	
Qy	466	TCCAGAGACACTCTGGGGGCGACACGGCGCGCTGGCTGGTCAAGAGTACTTCCCG	525	
Db	515	TCCAGAGACACTCTGGGGGCGACACGGCGCGCTGGCTGGTCAAGAGTACTTCCCG	574	
Qy	526	GAAAGGTCAGCGGTGTGTGAATCTAGGCGCCCTGACACAGCGCGTGCACACTTCCCG	585	
Db	575	GAAAGGTCAGCGGTGTGTGTGAATCTAGGCGCCCTGACACAGCGCGTGCACACTTCCCG	634	
Qy	586	GCTGTCTCACTCTCTCCAGGACTCACTCTCCAGAGGCTGATACCGTGGCCCTCCAGC	645	
Db	635	GCTGTCTCACTCTCTCCAGGACTCACTCTCCAGAGGCTGATACCGTGGCCCTCCAGC	694	
Qy	646	ACCTTGGGACCCAGCACTACATCTGCAACGTGAATCAACAGCCAGCAACCAAGGTG	705	
Db	695	ACCTTGGGACCCAGCACTACATCTGCAACGTGAATCAACAGCCAGCAACCAAGGTG	754	
Qy	706	GACAAAGAAAGTTGAGGCCAATCTTGTGTGACAAAACTCACAT	748	
Db	755	GACAAAGAAAGTTGAGGCCAATCTTGTGTGACAAAACTCACAT	797	
RESULT	3			
AR000007	AR000007	9209 bp	DNA	PAT
LOCUS	AR000007	9209 bp	DNA	04-DEC-1998
DEFINITION	Sequence 3 from patent US 5736137.			
ACCESSION	AR000007			
VERSION	AR000007.1	GI:3962538		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 9209)			
AUTHORS	Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and Rastetter,W.H.			
TITLE	Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma			
JOURNAL	Patent: US 5736137-A 3 07-APR-1998;			
FEATURES	Location/Qualifiers			
source	1..9209			
BASE COUNT	2239 a	2397 c	2390 g	2183 t
ORIGIN	/organism="unknown"			

Best Local Similarity 78.2%; Pred. No. 9.1e-103;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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Db 2401 ATGGGTGGAGCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
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Db 2461 GTACAACTGCAAGCCGCGGGCTGAGCTGGGAGCCCTGGGGCTCAGTGAAGTGTCC 2520
QY 121 TGTAAAGCTAGCGGTATATTTTCTAATTATGGAATCAATGGGCGGTATTTTTC 180
Db 2521 TGTAAAGCTAGCGGTATATTTTCTAATTATGGAATCAATGGGCGGTATTTTTC 2580
QY 181 GGGGAGGGCCGTGGAATGGATGGTGAATCTTACCGGGCTCTGAGACCCCAATATACC 240
Db 2581 GGTGCGGGCCGTGGAATGGATGGTGAATCTTACCGGAAATGGTGAATCTTCAAT 2640
QY 241 GAAATTTTAAAGACCGGTATATTTTCTAATTATGAGCGGTGACACTGAGTATACATG 300
Db 2641 CAGAAATTTCAAGGCAAGGCCACATTTGACTGAGACAAATCTCCAGCAGACCTACATG 2700
QY 301 GAGCTTCCAGCTTCCGATCGGAGACAGCGCCCTATATTTGCGCGGTATTTTTC 360
Db 2701 CAGCTCAGACCTGACATCTGAGGACTCTCGGCTATCTACTGTGCAAGATCGACTT-- 2758
QY 361 GGTCTAGCCCGAANTGTATTTTGTATTTGGGTCAAGAAACCTGTCACTGTCTCG 420
Db 2759 -ACTAGCGCGGTGACTGTACTTCAATGTCTGGGGCGCAGAGCACGCTCCCTCT 2817
QY 421 AGCCCTCCACCAAGGGCCCATCGGCTTCCCTCGGGCCCTCCCAAGACACCTCT 480
Db 2818 GCAGCTAGCAGCAAGGGCCCATCGGCTTCCCTCGGGCCCTCCCAAGACACCTCT 2877
QY 481 GGGGGCAGACGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAAACGGGTGACGGTG 540
Db 2878 GGGGGCAGACGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAAACGGGTGACGGTG 2937
QY 541 TCGTGAACCTCAGGCGCCCTGACCAAGGGCGTGCACACTTCCGGGCTCTTACAGTCC 600
Db 2938 TCGTGAACCTCAGGCGCCCTGACCAAGGGCGTGCACACTTCCGGGCTCTTACAGTCC 2997
QY 601 TCAGAGCTACTCTCTCAGCAGCGGTGGTGAACCTGCTCCAGCAGGTTGGGCAACCGAG 660
Db 2998 TCAGAGCTACTCTCTCAGCAGCGGTGGTGAACCTGCTCCAGCAGGTTGGGCAACCGAG 3057
QY 661 ACCTACATCTGCAAGTGAATCACAAGCCCAAGCAACCAAGGTGAGCAAGTGTGAG 720
Db 3058 ACCTACATCTGCAAGTGAATCACAAGCCCAAGCAACCAAGGTGAGCAAGTGTGAG 3117
QY 721 CCCAAATCTTGTGACAAACTCAGACAT 748
Db 3118 CCCAAATCTTGTGACAAACTCAGACAT 3145
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RESULT 4
LOCUS AR015961 9209 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776456.
ACCESSION AR015961
VERSION AR015961.1 GI:3972238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9209)
AUTHORS Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and Rastetter,W.H.
TITLE Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma
JOURNAL Patent: US 5776456-A 2 07-JUL-1998;

FEATURES
source Location/Qualifiers
1..9209
BASE COUNT 2238 a 2395 c 2394 g 2182 t
ORIGIN

Query Match 63.5%; Score 476; DB 9; Length 9209;
Best Local Similarity 78.2%; Pred. No. 9.1e-103;

Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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Db 2401 ATGGGTGGAGCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
QY 61 GTCCAACTGTGCAATCCGGCCGAGGTCAAGAACGCCAGGCTCAGTCAAGTGTCC 120
Db 2461 GTACAACTGCAAGCCGCGGGCTGAGCTGGGAGCCCTGGGGCTCAGTGAAGTGTCC 2520
QY 121 TGTAAAGCTAGCGGTATATTTTCTAATTATGGAATCAATGGGCGGTATTTTTC 180
Db 2521 TGTAAAGCTAGCGGTATATTTTCTAATTATGGAATCAATGGGCGGTATTTTTC 2580
QY 181 GGGGAGGGCCGTGGAATGGATGGTGAATCTTACCGGGCTCTGAGACCCCAATATACC 240
Db 2581 GGTGCGGGCCGTGGAATGGATGGTGAATCTTACCGGAAATGGTGAATCTTCAAT 2640
QY 241 GAAATTTTAAAGACCGGTATATTTTCTAATTATGAGCGGTGACACTGAGTATACATG 300
Db 2641 CAGAAATTTCAAGGCAAGGCCACATTTGACTGAGACAAATCTCCAGCAGACCTACATG 2700
QY 301 GAGCTTCCAGCTTCCGATCGGAGACAGCGCCCTATATTTGCGCGGTATTTTTC 360
Db 2701 CAGCTCAGACCTGACATCTGAGGACTCTCGGCTATCTACTGTGCAAGATCGACTT-- 2758
QY 361 GGTCTAGCCCGAANTGTATTTTGTATTTGGGTCAAGAAACCTGTCACTGTCTCG 420
Db 2759 -ACTAGCGCGGTGACTGTACTTCAATGTCTGGGGCGCAGAGCACGCTCCCTCT 2817
QY 421 AGCCCTCCACCAAGGGCCCATCGGCTTCCCTCGGGCCCTCCCAAGACACCTCT 480
Db 2818 GCAGCTAGCAGCAAGGGCCCATCGGCTTCCCTCGGGCCCTCCCAAGACACCTCT 2877
QY 481 GGGGGCAGACGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAAACGGGTGACGGTG 540
Db 2878 GGGGGCAGACGGCCCTGGGCTGCTGTCAAGGACTACTTCCCGAAACGGGTGACGGTG 2937
QY 541 TCGTGAACCTCAGGCGCCCTGACCAAGGGCGTGCACACTTCCGGGCTCTTACAGTCC 600
Db 2938 TCGTGAACCTCAGGCGCCCTGACCAAGGGCGTGCACACTTCCGGGCTCTTACAGTCC 2997
QY 601 TCAGAGCTACTCTCTCAGCAGCGGTGGTGAACCTGCTCCAGCAGGTTGGGCAACCGAG 660
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QY 661 ACCTACATCTGCAAGTGAATCACAAGCCCAAGCAACCAAGGTGAGCAAGTGTGAG 720
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QY 721 CCCAAATCTTGTGACAAACTCAGACAT 748
Db 3118 CCCAAATCTTGTGACAAACTCAGACAT 3145
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RESULT 5
LOCUS AR060920 9209 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5843439.
ACCESSION AR060920
VERSION AR060920.1 GI:5988611
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

QY 661 ACCTACATCTGCAACGTGATACACAGCCCAACACCAAGGTGGACAGAACTTGAG 720
DB 3058 ACCTACATCTGCAACGTGATACACAGCCCAACACCAAGGTGGACAGAACTTGAG 3117
QY 721 CCCAAATCTGTGTGACAAACTCAGACAT 748
DB 3118 CCCAAATCTGTGTGACAAACTCAGACAT 3145

RESULT 7
AR051652
LOCUS AR051652 18986 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5830698.
ACCESSION AR051652
VERSION AR051652.1 GI:5975016
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18986)
AUTHORS Refl,M.E., Barnett,R.Spence and McLachlan,K.Retla.
TITLE Method for integrating genes at specific sites in mammalian cells
JOURNAL via homologous recombination and vectors for accomplishing the same
FEATURES Patent: US 5830698-A 2 03-NOV-1998;
Location/Qualifiers
source 1..18986
BASE COUNT 4744 a 4958 c 4766 g 4518 t
ORIGIN

Query Match 63.5%; Score 476; DB 9; Length 18986;

Best Local Similarity 78.2%; Pred. No. 8.2e-103; Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGAAGCTGGGTATTCCTCTCTCTGTCAGTACTCGCGCTCCATCCCA 60
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QY 61 GTCCAACTGTGGCAATCCGGCGAGGTCAAGAACCGAGGGCTCAAGTAATGTCC 120
DB 9493 GTAACTGTGACAGCTGGGGGTGAGCTGTGAAGCTGGGGCTCAAGTAATGTCC 9552
QY 121 TGTAAAGCTAGCGCTATATTTTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 9553 TGCAGGCTTCTGTGCTACATTTTACCATATATGCACTGGGTAAACAGACACT 9612
QY 181 GGGCAGGCGCTGGAATGGAGTGGTGAATCTTACCGGGCTGTGTAGACCGAATATAC 240
DB 9613 GGTGCGGGCTGGAATGGATGGATGAGTATTTATCCCGGAATGGTATATCTCTACAT 9672
QY 241 GAAATTTTAAAGCCGTGTATATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
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QY 361 GGTTCAGCCCGAATTTGATTTTGTGGGTCAAGAACCGTGTACTGTCTCG 420
DB 9791 -ACTACGCGGCTGACTGTACTTCAATGTCTGGGGCGAGGACACAGCTACCTCTCT 9849
QY 421 AGGCGCTCCACCAAGGCGCCATCGGTCTCTCCCTGCGCGCTCTCTCAAGACACCTCT 480
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QY 481 GGGGCGACACGCGCTCTGGGTCTCTGCTCAAGACTCTCTCCGAGACGGTGAAGGTG 540
DB 9910 GGGGCGACACGCGCTCTGGGTCTCTGCTCAAGACTCTCTCCGAGACGGTGAAGGTG 9969
QY 541 TCGTGAAGTCAAGCGCCCTGACAGCGGCGTGCACACCTTCCGGGCTGTCTACAGTCC 600
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DB 9970 TCGTGAAGTCAAGCGCCCTGACAGCGGCGTGCACACCTTCCGGCTGTCTACAGTCC 10029
QY 601 TCAGACTCTACTCCCTCAGCAGGTGTGACCGTGGCTCTCAGACACTTGGGCAACCAG 660
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QY 661 ACCTACATCTGCAACGTGATACACAGCCCAACACCAAGGTGGACAGAACTTGAG 720
DB 10090 ACCTACATCTGCAACGTGATACACAGCCCAACACCAAGGTGGACAGAACTTGAG 3117
QY 721 CCCAAATCTGTGTGACAAACTCAGACAT 748
DB 10150 CCCAAATCTGTGTGACAAACTCAGACAT 3145

RESULT 8
AR092290
LOCUS AR092290 18986 bp DNA PAT 08-SEP-2000
DEFINITION Sequence 2 from patent US 5998144.
ACCESSION AR092290
VERSION AR092290.1 GI:10019044
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18986)
AUTHORS Refl,M.E., Barnett,R.Spence and McLachlan,K.Retla.
TITLE Method for integrating genes at specific sites in mammalian cells
JOURNAL via homologous recombination and vectors for accomplishing the same
FEATURES Patent: US 5998144-A 2 07-DEC-1999;
Location/Qualifiers
source 1..18986
BASE COUNT 4744 a 4958 c 4766 g 4518 t
ORIGIN

Query Match 63.5%; Score 476; DB 9; Length 18986;

Best Local Similarity 78.2%; Pred. No. 8.2e-103; Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGAAGCTGGGTATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
DB 9433 ATGGGTTGGAGCCCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 9492
QY 61 GTCCAACTGTGGCAATCCGGCGAGGTCAAGAACCGAGGGCTCAAGTAATGTCC 120
DB 9493 GTAACTGTGACAGCTGGGGGTGAGCTGTGAAGCTGGGGCTCAAGTAATGTCC 9552
QY 121 TGTAAAGCTAGCGCTATATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 9553 TGCAGGCTTCTGTGCTACATTTTACCATATATGCACTGGGTAAACAGACACT 9612
QY 181 GGGCAGGCGCTGGAATGGAGTGGTGAATCTTACCGGGCTGTGTAGACCGAATATAC 240
DB 9613 GGTGCGGGCTGGAATGGATGGATGAGTATTTATCCCGGAATGGTATATCTCTACAT 9672
QY 241 GAAATTTTAAAGCCGTGTATATTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
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QY 301 GAGCTCTCAGCCCTGCAATGGAGACAGCGCTCTATTTATTTGCGCGCTATTTT 360
DB 9733 CAGCTCAGAGCCCTGCAATGGAGACTCTGCGGTCTTACTGTGCAAGATGACTT-- 9790
QY 361 GGTTCAGCCCGAATTTGATTTTGTGGGTCAAGAACCGTGTACTGTCTCG 420
DB 9791 -ACTACGCGGCTGACTGTACTTCAATGTCTGGGGCGAGGACACAGCTACCTCTCT 9849
QY 421 AGGCGCTCCACCAAGGCGCCATCGGTCTCTCCCTGCGCGCTCTCTCAAGACACCTCT 480
DB 9850 GCAGCTAGCAACCAAGGCGCCATCGGTCTCTCCCTGCGCGCTCTCTCAAGACACCTCT 9909
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0Y	481	GGGGGACAGCGGCGCTGGGCTGCTGTGTCAGAGACTACTTCCCGCAACGGGTGACGGTG	540
Db	9910	GGGGGACAGCGGCGCTGGGCTGCTGTGTCAGAGACTACTTCCCGCAACGGGTGACGGTG	9969
0Y	541	TGCTGGAACTCAGGGGGCCCTGACACAGCGGCGGTGACACTTCCCGGCTGTCTACAGTCC	600
Db	9970	TGCTGGAACTCAGGGGGCCCTGACACAGCGGCGGTGACACTTCCCGGCTGTCTACAGTCC	10029
0Y	601	TCAGAGACTTACTCCCTCGACGACGCTGTGAGACCTGTCGTCGCTCCAGCAGCTTGGGACCCAG	660
Db	10030	TCAGAGACTTACTCCCTCGACGACGCTGTGAGACCTGTCGTCGCTCCAGCAGCTTGGGACCCAG	10089
0Y	661	ACCTACATCTGCAACGCTGATCACAAGCCGACCAACCCAAAGGTGACAAAGATTGAG	720
Db	10090	ACCTACATCTGCAACGCTGATCACAAGCCGACCAACCCAAAGGTGACAAAGATTGAG	10149
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Db	10150	CCCAATCTGTGACAAACTCACCAT	10177
RESULT	9		
LOCUS	AR038306	3282 bp	DNA
DEFINITION	Sequence 154 from patent US 5804440.		PAT
ACCESSION	AR038306		29-SEP-1999
VERSION	AR038306.1	GI:5957023	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 3282)		
AUTHORS	Burton,D.R., Barbas,C.F. and Lerner,R.A.		
TITLE	Human neutralizing monoclonal antibodies to human immunodeficiency virus		
JOURNAL	Patent: US 5804440-A 154 08-SEP-1998;		
FEATURES	Location/Qualifiers		
source	1..3282		
BASE COUNT	710 a 1109 c 864 g 599 t		
ORIGIN	/organism="unknown"		
	1..3282		
Query Match	62.3%;	Score 467.4;	DB 9; Length 3282;
Best Local Similarity	78.7%;	Pred. No. 1.2e-100;	
Matches 577; Conservative	0;	Mismatches 141;	Indels 15; Gaps 1
0Y	1	ATGAAGTGGAGCTGGGTTATTCTTCTTCTCTCTGTCAGTACTGCGGCGTCCACTCCCAA	60
Db	15	ATGAAGTGGAGCTGGGTTATTCTTCTTCTCTCTGTCAGTACTGCGGCGTCCACTCCCAA	74
0Y	61	GGCAACTGGTGCANCCGCGGCGCGGAGTCAGAAAGCCGAGGGGCTTCATCAAGGTGTC	120
Db	75	GTTCCAGCTGCTTCACTGTCGCGGCTGAGGTGAAGAAAGCCGAGGGGCTTCATCAAGGTGTC	134
0Y	121	TGTAAAGCTACGCGCTATATTTTCTTAATTAATGATTCATATGGGTGCGTACAGCCCCC	180
Db	135	TGTCAAGGCTTTCGATATACGATTCAGTACTTGTATTATTCATTTGGGTGGCCAGGCCCC	194
0Y	181	GGGCAAGGCGCTGGAATGATGATGGGTGAGATCTTACCGGGCTTGTTGAGCACCGAATATAC	240
Db	195	GGACAGAGGTTTGAATGATGATGATGATGATCAATCCCTTACACAGGAAACAAAGAAATTTCA	254
0Y	241	GAAATTTTAAAGACCGCTGTACTTATGACAGCGTCGACACTTGCACATAGTACATATACAG	300
Db	255	GCGAAGTTCACAGACAGATCACCTTATCGGCGGACACATCCGCGAACACAGCTTACATG	314
0Y	301	GAGCTCTCCAGCGCTGCATCGAGACACAGCGCGCTATATTATTTGCGCG	348
Db	315	GAGTTGAGAGAGCGCTCAGAGCTGTCAGACAGCGCTGTTTATTATTGTGCCGAGATGGGCCA	374
0Y	349	---CGTTATTTTTTTTGGTTCTAGCCCGAAATGTGATTTTGAATGTTGGGTCAAGGACC	405

Db	375	TATAGTGGGATGATTTCTCCCGAGGCACATTATTATATGACGTGTGGGGCAAAAGAAC	434
OY	406	CTGGATCAGTGTCTGAGGGGCGCTCCACCAAGGGGCCATCGATCTTCCCTGGCGCCCTCC	465
Db	435	ACGGTCATCTGTAGCTCAAGCTTCCACCAAGGGGCCATGGGTCTTCCCTTGGACCCCTCC	494
OY	466	TCCAAAGAGACCTCTGGGGGGGCACAGCGGCCCTGGGGCTCTGTGTCAAGACTACTTCC	525
Db	495	TCCAAAGAGACCTCTGGGGGGGCACAGCGGCCCTGGGGCTCTGTGTCAAGACTACTTCC	554
OY	526	GAACCGGTGACGGGTCTCTGGAACTCAGGGGCCCTGACACAGCGGTGCACACCTTCCG	585
Db	555	GAACCGGTGACGGGTCTCTGGAACTCAGGGGCCCTGACACAGCGGTGCACACCTTCCG	614
OY	586	GCTGTCTCAAGACTCTCTAGAGACTCTACTCCCTCAGACAGCTGTGTACCGTCCCTCAGC	645
Db	615	GCTGTCTCAAGACTCTCTCAGAGACTCTACTCTCCTCAGCACAGCGTGTACCGTCCCTCAGC	674
OY	646	AGCTTGGGACCCAGACCTTACTCTGTCAACGTGAATCAAGGCCAGCACACCAAGGTG	705
Db	675	AGCTTGGGACCCAGACCTTACTCTGTCAACGTGAATCAAGGCCAGCACACCAAGGTG	734
OY	706	GACAGAAAGTTG 718	
Db	735	GACAGAAAGTTG 747	

RESULT	10
AR038320/c	
LOCUS	
DEFINITION	AR038320
ACCESSION	Sequence 169 from patent US 5804440.
VERSION	AR038320
KEYWORDS	AR038320.1 GI:5957037
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unknown.
AUTHORS	Unclassified.
TITLE	1 (bases 1 to 3282)
JOURNAL	Burton,D.R., Barbas,C.F. and Lerner,R.A.
FEATURES	Human neutralizing monoclonal antibodies to human immunodeficiency virus Patent: US 5804440-A 169 08-SEP-1998; Location/Qualifiers 1..3282 "/organism='unknown'"
BASE COUNT	599 a 864 c 1109 g 710 t
ORIGIN	

Query Match	62.3%;	Score 467.4;	DB 9;	Length 3282;
Best Local Similarity	78.7%;	Pred. No. 1.2e-100;		
Matches 577;	Conservative	0;	Mismatches 141;	Indels 15; Gaps 1;
QY 1	ATGAGTGGAGCTGGGTATTCCTTCCTCCCTGTGTAGTAACCTCCCGCGCTCCACATCCCAA	60		
DB 3268	ATGGATGGAGCTGGGTCTTCTCTCTCTCCCTGTGTAGTAACCTCCCGCGCTCCACATCCCAA	3209		
QY 61	GTCCAACTGGTGCATCCGCGCGCGCGGCAAGCAACCCAGCGCCCTCAGTCAAAGTGTC	120		
DB 3208	GTTCAGCTGTGTACAGTCCGCGCGCGGTGAGGGAAGCAACCTCGGGGCTCAGTGAAGTTTCT	3149		
QY 121	TGTAAAGTACAGCGGCTATATTTTTCCTTAATTAATGATTCAATGGGTGGCTCAGGCCCC	180		
DB 3148	TGTCAAGCTTCTGGATACAGATTCACTAATCTTTGTTATTCATTTGGTGGCCAGGCCCCC	3089		
QY 181	GGGCAAGGCGCTGGAATGGATGGGTGAGATCTTAACCGGGCTTGGTAGCACCGAATATPAC	240		
DB 3088	GGCAAGAGTTTGATGATGGATGGGATGAGATCAATCTTTACACGGAAACAAAGATTTC	3029		
QY 241	GAAATTTTAAAGACCGGTTTACTATAGACCGGTGACACTTCGACTATGTAATATCAG	300		
DB 3028	GGAGATTCACAGACAGATCTACCTTTACCGGGGACACATCCGCGCAACACAGCTTCAG	2969		

QY 301 GAGCTTCACAGCTCGATGGAGAGACAGCGCCCTATATTATGCGC----- 348
 Db 2968 GAGTTGAGAGAGCTCAGCTGAGACAGCGCTTATTATTGCGAGAGTGGGGCA 2909
 QY 349 ---CGTTATTTTGGTTCTAGCCCAATTTGATTTTGTGTTGGGCTCAAGAAC 405
 Db 2908 TATAGTTGGGATGATTTCTCCAGAGCAATTTATATGAGCTGGGGCAAGAAC 2849
 QY 406 CTGATCACTGCTTCAGACAGCGCCCTCCAGAGGAGGAGGCTTCCTCCCGGCGCC 465
 Db 2848 AGGTGATCTGAGACTAGCTTCCAGCAAGGCGCCATCGTCTCCCTGACACCTCC 2789
 QY 466 TCCAGAGACACTCTTGGGGGACAGCGCCCTGGGCTGCTGATCAAGACTATTTCCC 525
 Db 2788 TCCAGAGACACTCTTGGGGGACAGCGCCCTGGGCTGCTGATCAAGACTATTTCCC 2729
 QY 526 GAACCGGTGACGTTGTGTGGAATCAGGCGCCCTGACACGCGGCTGACACCTTCCC 585
 Db 2728 GAACCGGTGACGTTGTGTGGAATCAGGCGCCCTGACACGCGGCTGACACCTTCCC 2669
 QY 586 GCTGTCTACAGTCTCAGAGACTACTCTCCCTCAGACAGCGGCTGACCGCTCCAGC 645
 Db 2668 GCTGTCTACAGTCTCAGAGACTACTCTCCCTCAGACAGCGGCTGACCGCTCCAGC 2609
 QY 646 AGCTTGGGACCCAGACCTACATCTGCAACGTGATCAACAAGCCAGACACCAAGGTG 705
 Db 2608 AGCTTGGGACCCAGACCTACATCTGCAACGTGATCAACAAGCCAGACACCAAGGTG 2549
 QY 706 GACAGAAAGTTG 718
 Db 2548 GACAGAAAGTTG 2536

RESULT 11
 LOCUS 158595 3282 bp DNA PAT 07-OCT-1997
 DEFINITION Sequence 154 from patent US 5652138.
 ACCESSION 158595
 VERSION 158595.1 GI:2477833
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3282)
 AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
 TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus
 JOURNAL Patent: US 5652138-A 154 29-JUL-1997;
 FEATURES
 source 1.3282
 Location/Qualifiers
 BASE COUNT 710 a 1109 c 864 g 599 t
 ORIGIN

Query Match 62.3%; Score 467.4; DB 10; Length 3282;
 Best Local Similarity 78.7%; Pred. No. 1.2e-100;
 Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;
 QY 1 ATGAAGTGAAGCTGGGTATTTCTTCTCTCTCTGCACTAGTACGCGGCTCCACCTCCAA 60
 Db 15 ATGAATGAGCTGGGTCTTCT 74
 QY 61 GTCCAACTGTGTCATCCGCGCGGAGGTCAAGAGCCAGGCGCTCAGTCAAAAGTCTC 120
 Db 75 GTTCACCTGTGTCATCCGCGCGGAGGTCAAGAGCCAGGCGCTCAGTCAAAAGTCTCT 134
 QY 121 TGTAAAGCTAGCGGTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 180
 Db 135 TGTCAAGCTTCTGATACATTCAGTACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 194
 QY 181 GGGCAGGCGCTGGAATGATGGGTGAGATCTTACGGGCTCTGTAGACCGAATATACC 240

Db 195 GGACAGAGGTTTGAATGATGGGATGATCAATCTTACACGGAACAAAGATTTTCA 254
 QY 241 GAAATTTAAAGACCGTCTTATGAGCGGTGACACTTCGACTGTACATATACATG 300
 Db 255 GCGAAGTTCAGAGACGATGACCTTACCGGACACATTCGCGGACACAGCTTACATG 314
 QY 301 GAGCTCTCCAGCTCGATCGAGAGACAGCGGCTCTATATTATGCGC----- 348
 Db 315 GAGTTGAGAGAGCTCAGGCTCTGAGACAGCGGCTTATTATTATGTCAGAGTGGGGCA 374
 QY 349 ---CGTTATTTTGGTTCTAGCCCAATTTGATTTTGTGTTGGGCTCAAGAAC 405
 Db 375 TATAGTTGGGATGATTTCTCCAGAGCAATTTATATGAGACTCTGGGCAAGAAC 424
 QY 406 CTGATCACTGCTTCAGAGCGCCCTCCAGAGGAGGAGGCTTCCTCCCGGCGCCCTCC 465
 Db 435 AGGTGATCTGAGCTACACTTCCAGCAAGGCGCCATCGTCTCCCTGACACCTTCC 494
 QY 466 TCCAGAGACACTCTTGGGGGACAGCGCCCTGGGCTGCTCAAGACTATTTCCC 525
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 QY 526 GAACCGGTGACGTTGTGTGGAATCAGGCGCCCTGACACGCGGCTGACACCTTCCC 585
 Db 555 GAACCGGTGACGTTGTGTGGAATCAGGCGCCCTGACACGCGGCTGACACCTTCCC 614
 QY 586 GCTGTCTACAGTCTCAGAGACTACTCTCCCTCAGACAGCGGCTGACCGCTCCAGC 645
 Db 615 GCTGTCTACAGTCTCAGAGACTACTCTCCCTCAGACAGCGGCTGACCGCTCCAGC 674
 QY 646 AGCTTGGGACCCAGACCTACATCTGCAACGTGATCAACAAGCCAGACCAAGGTG 705
 Db 675 AGCTTGGGACCCAGACCTACATCTGCAACGTGATCAACAAGCCAGACCAAGGTG 734
 QY 706 GACAGAAAGTTG 718
 Db 735 GACAGAAAGTTG 747

RESULT 12
 LOCUS 158609/c 3282 bp DNA PAT 07-OCT-1997
 DEFINITION Sequence 169 from patent US 5652138.
 ACCESSION 158609
 VERSION 158609.1 GI:2477847
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3282)
 AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
 TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus
 JOURNAL Patent: US 5652138-A 169 29-JUL-1997;
 FEATURES
 source 1.3282
 Location/Qualifiers
 BASE COUNT 599 a 864 c 1109 g 710 t
 ORIGIN

Query Match 62.3%; Score 467.4; DB 10; Length 3282;
 Best Local Similarity 78.7%; Pred. No. 1.2e-100;
 Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;
 QY 1 ATGAAGTGAAGCTGGGTATTTCTTCTCTCTCTGCACTAGTACGCGGCTCCACCTCCAA 60
 Db 3268 ATGAATGAGCTGGGTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3209
 QY 61 GTCCAACTGTGTCATCCGCGCGGAGGTCAAGAGCCAGGCGCTCAGTCAAAAGTCTC 120
 Db 3208 GTTCACCTGTGTCATCCGCGCGGAGGTCAAGAGCCAGGCGCTCAGTCAAAAGTCTCT 3149

[illegible]


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257: gb_est188:*
258: gb_est189:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

[illegible]

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Db      569 TCGTGAACACGAGCGCCCTGACCAAGCGCGTGCACACCTTCCGGCTGCTCTACAGTC 628
QY      601 TCAGACTCTACTCCCTCAGCAGCGGTGGTGGACCGCGCCCTCAGCAGGCTGGGACCCAG 660
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Db      629 TCAGAGCTCTACTCTCCCTCAGCAGCGGTGGTGGACCGCGCCCTCAGCAGGCTGGGAC 687
QY      661 ACCTACATCTGCAACGTGAATCAGAACGCCAGCAACACCAAGTGAGACAGAAAGTTGAG 720
        |||||
Db      688 AACACATCTGCAACGTGAATCAGAAC--CCAGCAACACCAAG--GGAGAGAAAGTTGAG 744
QY      721 CCCAAATCTGTGACAAA 739
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Db      745 AATCTGTGTGACAAA 761

RESULT  2
LOCUS   BF342599      783 bp      mRNA      EST      22-NOV-2000
DEFINITION 602013731F1 NCI.CGP.Brn64 Homo sapiens cDNA clone IMAGE:4149679
ACCESSION BF342599
VERSION   BF342599.1 GI:11289621
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 783)
AUTHORS  NIH-MGC http://mgc.ncl.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-r@mail.nih.gov
           Tissue Procurement: David N. Louis, M.D.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.llnl.gov
           Plate: LLM6411 row: m column: 08
           High quality sequence stop: 744.
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               /clone="IMAGE:4149679"
               /clone_lib="NCI_CGAP_Brn64"
               /tissue_type="glioblastoma with EGFR amplification"
               /lab_host="DH10B (T1 phage-resistant)"
               /note="Organ: brain; Vector: PCMV-SPORT6; Site: 1; NotI:
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               Average insert size 1.57 kb. Constructed by Life
               Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT  185 a      235 c      209 g      154 t

ORIGIN
Query Match      53.3%; Score 399.8; DB 147; Length 783;
Best Local Similarity 76.8%; Pred. No. 1.8e-102;
Matches 509; Conservative 0; Mismatches 137; Indels 17; Gaps 1;

Db      103 GCCCAGCTCAAGTGTCTGTAAGCTAGCGGCTATATATTTTCTATATTTGATTC 162
QY      163 TGGGTGCGTACAGCCCCCGGCGAGGCGCTGGAATGATGGGTGAGATCTTACGGGCTCT 222
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Db      66 TGGGTGCGGAGCGGTCCAGGAGGGGCTGAGTGGCGAGTATATATGATATGATGA 125
QY      223 GGTAGACCGGATATACCGAAATTTTAAGACCGGTGTTACTATGACCGGTGACACTTCG 282
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Db      126 AGTAAATCAATACTACAGACTCCGTGAAGGGCGGATTCACCGTCTCAAGAGACATGTT 185

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QY      283 ACTAGTACAGTATACATGAGACTCTCCAGCTCGATCGAGAGACAGCGCGTCTATTAT 342
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Db      186 AAAAATATGTTGATATGCAAAATGAACAGCGCTGAGAGCCAGGACAGCGCTGATATAT 245
QY      343 TGGCGCG-----TTATTTTGGTTCTAGCCGAATTTGTTTGG 385
        |||||
Db      246 TGTGCGAGAGGGAACAAAGAGTGTATTATGCTTCCCGCCCAAGAGAGCATGATGTTTG 305
QY      386 ATGTTGGGTGCAAGAACCTGTGCTACGTCTCGAGCGGCTCACCAGGCGCATCGG 445
        |||||
Db      306 ATATCTGGGGCCAGAGGACATGATGTCACGCTCTTCAGGCTCCACCAAGGCCATCGG 365
QY      446 TCTTCCCTGGGCGCCCTCTCCAGAGACACTCTGGGGGACAGAGCGGCTGGGCTGCC 505
        |||||
Db      366 TCTTCCCTGGGCGCCCTCTCCAGAGACACTCTGGGGGACAGAGCGGCTGGGCTGCC 425
QY      506 TGTGCAAGGACTACTTCCCGGAACCGGTGACGGTGTGTGTTGGAACCTCAGGCGCTGACCA 565
        |||||
Db      426 TGTGCAAGGACTACTTCCCGGAACCGGTGACGGTGTGTGGAACCTCAGGCGCTGACCA 485
QY      566 GCGGCGTGCACACACTTCCCGGCTGCTCTACAGTCCAGAGACTCTACTCCCTCAGACGC 625
        |||||
Db      486 GCGGCGTGCACACACTTCCCGGCTGCTCTACAGTCCAGAGACTCTACTCCCTCAGACGC 545
QY      626 TGTGACCGTGCACCGCTCAGAGAGCTGGGACCCAGACCTACTACTGCAACGTGAATCACA 685
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Db      546 TGTGACCGTGCACCGCTCAGAGAGCTGGGACCCAGACCTACTACTGCAACGTGAATCACA 605
QY      686 AGCCGACCAACCAAGGTGAGACAAGAAAGTTAGCCCAATCTTGTGACAAAATCTCACA 745
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Db      606 AGCCGACCAACCAAGGTGAGACAAGAGTTAGCCCAATCTTGTGACAAAATCTCACA 665
QY      746 CAT 748
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Db      666 CAT 668

RESULT  3
LOCUS   BG397867      860 bp      mRNA      EST      12-MAR-2001
DEFINITION 602438967F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565008 5',
ACCESSION BG397867
VERSION   BG397867.1 GI:13291315
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 860)
AUTHORS  NIH-MGC http://mgc.ncl.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.llnl.gov
           Plate: LLM1281 row: f column: 17
           High quality sequence stop: 846.
           Location/Qualifiers
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               /db_xref="taxon:9606"
               /clone="IMAGE:4565008"
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QY 511 AAGACTACTTCCCGCAACGGGTGCTGTGGAATCAGCGCCCTGACAGCGGC 570
DB 361 AAGACTACTTCCCGCAACGGGTGCTGTGGAATCAGCGCCCTGACAGCGGC 420
QY 571 GTGACACCTTCCCGGTGCTGTGGAATCAGCGCCCTGACAGCGGC 630
DB 421 GTGACACCTTCCCGGTGCTGTGGAATCAGCGCCCTGACAGCGGC 480
QY 631 ACCGTGCTTCCCGGTGCTGTGGAATCAGCGCCCTGACAGCGGC 690
DB 481 ACCGTGCTTCCCGGTGCTGTGGAATCAGCGCCCTGACAGCGGC 540
QY 691 AGCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGACAAAATCACAAT 748
DB 541 AGCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGACAAAATCACAAT 598

RESULT 5
BG397847 869 bp mRNA EST 12-MAR-2001
LOCUS BG397847
DEFINITION 602438939F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565192 5',
mRNA sequence.
ACCESSION BG397847
VERSION BG397847.1 GI:13291295
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Mammalia: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1281 row: n column: 09
High quality sequence stop: 805.
location/Qualifiers
1. 869
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4565192"
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library."

BASE COUNT 200 a 266 c 226 g 177 t
ORIGIN

Query Match 52.5%; Score 393.6; DB 153; Length 869;
Best Local Similarity 76.3%; Pred. No. 1e-100;
Matches 580; Conservative 0; Mismatches 159; Indels 21; Gaps 7;

QY 1 ATGAAGTGGAGCTGGTATTTCTTCTCTGTCAGTAAGTCCGGCGTCCATCCCAA 60
DB 44 ATGAAGTGGAGCTGGTATTTCTTCTCTGTCAGTAAGTCCGGCGTCCATCCCAA 103

QY 61 GTCCAACTGTGTCATCCGCGCCGAGTGCAGAGCCAGGGGCTCAGTCAAAATGTCC 120
DB 104 GTTCAGTGTGTCATCCGCGCCGAGTGCAGAGCCAGGGGCTCAGTCAAAATGTCC 163
QY 121 TGTAAAGTGAAGGCTATATTTTCTATATATATATATATATATATATATATAT 180
DB 164 TGTAAAGTGAAGGCTATATTTTCTATATATATATATATATATATATATATAT 223
QY 181 GGGCAGGGCTGGAATGATGATGGGTGATATCTTACCGGGGCTGTGTAGCAGCAATATAC 240
DB 224 GGAACAAGTGTGTCAGTGTGATGGATGATGATGATGATGATGATGATGATGATG 283
QY 241 GAAATATTTAAAGACCGTGTATATATATATATATATATATATATATATATAT 300
DB 284 CAGAA-CGTCCAGGACAGTACATACATGATGATGATGATGATGATGATGATGATG 342
QY 301 GAGCTCTCCAGCTGCGATCGGAGACAGGCGCGTCTATATATATGCGC----- 348
DB 343 GAACTGAGGAGCTGACATCTGACGACAGCG-CGTGTATATATATGTCAGAAATGAGGGCA 401
QY 349 ----CGTATATTTTGTGTTCTAGCCGCAATGTGATTTGATGTTGGGTCAAGAAC 405
DB 402 GCTCGTTCATTTTATTTTGGATTTCTCTATTTACTTTGATATATATGAGGCAAGG 461
QY 406 CTGTGTCAGTGTGAGCGCTTCACCAAGGCGCATGCTTCCCTGCGCCTCC 465
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QY 526 GAACCGGTGACGCTGTGTCAGTGTGTCAGTGTGTCAGTGTGTCAGTGTGTCAGTGTGTC 584
DB 581 GAACCGGTGACGCTGTGTCAGTGTGTCAGTGTGTCAGTGTGTCAGTGTGTCAGTGTGTC 640
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DB 641 GGGTGTCTTACAGTCTCTGAGACTACTCTCTGACAGCGGTGTGACCGCTCCCA 700
QY 644 GCAGCTTGGGACCCAGACTTACATCTGCAAGCTGATTCACAGCCAGCAACCAAG 703
DB 701 GCAGCTTGGGACCCAGACTTACATCTGCAAGCTGATTCACAGCCAGCAACCAAG 759
QY 704 TGGACAAGAAAGTTGAGCCCAATCTTGACAAAATCTCA 743
DB 760 TGGACAAGAAAGTTGAGCCCAATCTTGACAAAATCTCA 799

RESULT 6
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LOCUS BF664166
DEFINITION 602145969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309220 5',
mRNA sequence.
ACCESSION BF664166
VERSION BF664166.1 GI:11938061
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Mammalia: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 823)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LCM1183 row: 1 column: 17
High quality sequence stop: 750.
Location/Qualifiers

FEATURES

Source

1. 823
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 183 a 254 c 227 g 159 t
ORIGIN

Query Match 51.1%; Score 383.4; DB 151; Length 823;
Best Local Similarity 75.0%; Pred. No. 7.9e-98;
Matches 559; Conservative 0; Mismatches 176; Indels 10; Gaps 6;

OY 1 ATGAAGTGTAGGTGGTATTTCTCTCCCTCCCTGCTAGTACGCGCGGCTCCCA 60
DB 44 ATGGAAGTGTAGGTGGTATTTCTCTCCCTCCCTGCTAGTACGCGCGGCTCCCA 103
OY 61 GTCAAGTGTAGGTGGTATTTCTCTCCCTCCCTGCTAGTACGCGCGGCTCCCA 120
DB 104 GTTCAAGTGTAGGTGGTATTTCTCTCCCTCCCTGCTAGTACGCGCGGCTCCCA 163
OY 121 TGTAAAGTGTAGGTGGTATTTCTCTCCCTCCCTGCTAGTACGCGCGGCTCCCA 180
DB 144 TGTAAAGTGTAGGTGGTATTTCTCTCCCTCCCTGCTAGTACGCGCGGCTCCCA 223
OY 181 GGGCAGGCGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 224 GACACAGGCGCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 281
OY 241 GAAATTTTAAAGACCGTGTATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 282 ACAGAAAGTGTAGGTGGTATTTCTCTCCCTCCCTGCTAGTACGCGCGGCTCCCA 341
OY 301 GAGCTGTCCAGCGCTGGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 342 GAGCTGTCCAGCGCTGGATGATGATGATGATGATGATGATGATGATGATGAT 400
OY 361 GGTGTAG--CCGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 418
DB 401 AGTGTGTAGTGTACTGTACTGTACTGTACTGTACTGTACTGTACTGTACTGTACT 460
OY 419 CGAGGCGCTCCAGCAAGGCGCGCTGTCTCCCTGCGCGCTCCCAAGAGCACT 478
DB 461 C-CTGAGCTCCAGCAAGGCGCGCTGTCTCCCTGCGCGCTCCCAAGAGCACT 519
OY 479 CTGGGGGCGACAGCGCGCTGTCTCCCTGCGCGCTCCCAAGAGCACT 538
DB 520 CTGGGGGCGACAGCGCGCTGTCTCCCTGCGCGCTCCCAAGAGCACT 577
OY 539 TGTCTGTGAACTACAGCGCGCTGTCTCCCTGCGCGCTCCCAAGAGCACT 598
DB 578 TGTCTGTGAACTACAGCGCGCTGTCTCCCTGCGCGCTCCCAAGAGCACT 637
OY 599 CCTCAGGACTACTCTCCAGAGCGGTGACGCGCTCCCAAGAGCACT 658
DB 638 CCTCAGGACTACTCTCCAGAGCGGTGACGCGCTCCCAAGAGCACT 697
OY 659 AGACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGCAAGAACTTG 718

DB 698 AGACCTACATCTGCGACGTGATTCACAGCCGACGACACCAAG--TGCCCAAGAGTTG 755
OY 719 AGCCCAATCTGTGACAAAACCTCA 743
DB 756 AGCCCAATCTGTGAAATAATCACA 780

RESULT 7
BG398411 796 bp mRNA EST 12-MAR-2001
LOCUS 602439885F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4566236 5',
DEFINITION mRNA sequence.
ACCESSION BG398411 GI:13291859
VERSION BG398411
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 796)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs@remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov

plate: LCM1284 row: 1 column: 21
High quality sequence stop: 774.

FEATURES

Source

1. 796
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 174 a 256 c 215 g 151 t
ORIGIN

Query Match 50.9%; Score 381.4; DB 153; Length 796;
Best Local Similarity 75.9%; Pred. No. 2.9e-97;
Matches 503; Conservative 0; Mismatches 146; Indels 14; Gaps 2;

OY 98 CAGGGCGCTCAAGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTTAATATGGA 157
DB 2 CTGGGGGCTCCCTGAGACTCTCTCTGCGGCGCTGTGATTTGCAAAATGCA 61
OY 158 TTCAATGGGTGCGTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 217
DB 62 TGACCTGGGTCCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
OY 218 GCTGTGAGACCGCAATATACGAAATTTTAAGACCGGTGTACTATAGCGGTGACA 277
DB 122 ATGGCGCCAGTACATCTACAGAGACTCCGTAAGGCGCGCTTCAACATCTCCAGAGCA 181
OY 278 CTTCGACTAGTACATATACATGAGACTCTCCAGCCTCGCATCGAGAGACGCGCGTCT 337

[illegible]

directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-DNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library.*

Query Match	49.1%	Score 368.6	DB 153	Length 841
Best Local Similarity	70.7%	Pred. No. 1.2e-93		
Matches 521	Conservative 0	Mismatches 209	Indels 7	Gaps 2
QY 1	ATGAAGTGAGACGTGGGTTATTCCTCTCCCTGTGACGTAACGCGGGCTCACGTCCAA	60		
Db 22	ATGAAGACACGTGGTCTTCCTCCTCTGGGAGGACGTCACAGATGGGTCTGTCTGAG	81		
QY 61	GTCCAATCTGTGCAATCCGGCGCCGAGGTCAAGAACCAAGGGGCTCAGTCAAGTGTCC	120		
Db 82	GTACAGCTGCAGAGATCCGGGCCCAAGACTGTGGAAGCCTTCGGGGACCTGTCCCTCAC	141		
QY 121	TGTAAAGTACGCGCTATATTTTCTATATATTTGATTCATATGGGTGGTCAAGGCCCC	180		
Db 142	TGCGCTGTCTCTGGGCTCCATCAATGATATATATATATATATATATATATATATAT	201		
QY 181	GGGCGAGGCTCGAATGAGATGGGTGAGATCTTACCGGGCTGTGTAGACCAAGATATACC	240		
Db 202	GGGAAGGGGCTGTGAGTGTGATTTGGAGAAATCTAC---ATACTGTATAAACCAACTACAC	258		
QY 241	GAATAATTTTAAAGACCGTGTACTATATGACGCGCTGACACTTGCATAGTACATATACAG	300		
Db 259	CCGTCCCTCCGAGTGCAGTCAACCACTTTCACATAGAACAGTCCGACATATGATCTCCCG	318		
QY 301	GAGCTCTCCAGCCTGCGATCGGAGGACACGCGCTATATTTATTTATTTGCGCGGTTATTTT	360		
Db 319	AGGCTGACATCTGTGACCGCGGACACGCGCGTGTACTTCTGTGCGAGCA---TAT	374		
QY 361	GGTCTACCCGAAATTTGTATTTTGTATGTTTTGGGTCAAGAAACCTGTCTACTGTCTCG	420		
Db 375	GGGACTTACTGTGACACTCGGGGATTTTGACTACTAGGGGGCCAGGAACCTGTGTCAACGCTCC	434		
QY 421	AGCGCTTCACACAAAGGGGCCATCGGTCTTCCCGCTGGGGCCCTCCCTCCAAAGCACTCT	480		
Db 435	TCAGCTTCACACAAAGGGGCCATCGGTCTTCCCGCTGGGGCCCTCCCTCCAAAGCACTCT	494		
QY 481	GGGGCACAGCGGCGCTGTGCTGTGTCAAGACTACTTCCCGAAACCGGTGACGGTG	540		
Db 495	GAGAGCAAGCGGCGCTGTGCTGTGTCAAGACTACTTCCCGAAACCGGTGACGGTG	554		
QY 541	TGCTGGAACCTACAGCGGCGCTGTGACAGCGGCGGTGACACCTTCCCGGCTGTCTTACATTC	600		
Db 555	TGCTGGAACCTACAGCGGCGCTGTGACAGCGGCGGTGACACCTTCCCGGCTGTCTTACATTC	614		
QY 601	TCAGGACTCTACTCCCTTCAGAGCGGTGTGACACCGGCTCCCTCCAGGAGCTGGGACCCGAG	660		
Db 615	TCAGGACTCTACTCCCTTCAGAGCGGTGTGACACCGGCTCCCTCCAGGAGCTGGGACCCGAG	674		
QY 661	ACCTACATCTCAACGATGATCAAGAGCCAGCAACCAAGTGGAGACAAGATTTGAG	720		
Db 675	ACCTACATCTCAACGATGATGATCAAGAGCCAGCAACCAAGTGGAGACAAGATTTGAG	734		
QY 721	CCCAAACTTGTGACAA 737			
Db 735	CGCAAACTTGTGTGCA 751			

Accession	Version	GI
BF663151	1	GI:11937046
BF663151.1	1	GI:11937046
EST		
KEYWORDS		
SOURCE		
ORGANISM		
human.		
Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
NIH-MGC http://mgc.ncl.nih.gov/		
1 (bases 1 to 864)		
Unpublished (1999)		
Contact: Robert Strausberg, Ph.D.		
Email: c9apbs@email.nih.gov		
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
cDNA Library Preparation: Ling Hong/Rubin Laboratory		
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
DNA Sequencing by: Incyte Genomics, Inc.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:		
http://image.lnl.gov		
Plate: LNCMI180 row: b column: 19		
High quality sequence stop: 703.		
Location/Qualifiers		
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/clone_1db="NIH_MGC_48"		
/tissue_type="Primary B-cells from tonsils (cell line)"		
/lab_host="DH10B (phage-resistant)"		
/note="Organ: B-cells; Vector: pOH7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."		
BASE COUNT		
191 a 264 c 242 g 167 t		
ORIGIN		
Query Match	48.7%	Score 365; DB 151; Length 864;
Best Local Similarity	75.4%	Ident. No. 1.3e-92;
Matches 494; Conservative	0; Mismatches 155; Indels	6; Gaps
1 ATGAGTGGAGTGGGTATTCTCTCCCGCTGAGTAACGCGGCGTCCAGTCCCA 60		
47 ATGAGTGGAGTGGGTATTCTCTCTCTTTGTGTGGACGACGATCAAGTGTCCAAATCCCA 106		
61 GTCAACTGTGTGCAATCCGCGCGCCGAGGTCAAGAAAGCGGGGCTTCAGTCAAAGTGTCC 120		
107 GTCCAGCTGTGTGCAATCTGTGGGCTGAGGTGAAGAAAGCTGGGCTCCATTAAGGTCTCC 166		
121 TGTAAAGTACGCGGTATATTTTCTATTAATTGATTCATTTGGTGGTGTAGCGCCCC 180		
167 TGTCAAGGCTTCTGTGAGGACCTCTCAATAGGTATGCAATCACTGCGCGGAGAGGCGCTT 226		
181 GGGCAGGCGCTGATGATGTGGTGTGATCTTAACGGGCTGTGTGATGACGCAATATATAC 240		
227 GGACAGAGGCTGTGATGTGATGGGGGATGACGCTTTCTTTTGGAGAAACCAACTATACGA 286		
241 GAAATTTTAAAGACCGTGTACTTGTGACGCGGTACACTTGCATAGTACATATATCATG 300		
287 CAGAGTTCACGAGGAGGTCTTATTTACCGGGGACGAATCCACGACGACGACCTTATG 346		
301 GAGCTCTCCAGCTCGATCGAGGACAGCGCGCTCTATTATTTGGCGCGGTATTATTT--T 357		
347 GAGGTGACACGCTGATGATCTGAACAGACGCGCATTTTATTTACTGTGTGACGATCACGTGGCC 406		
358 TTTGGTCTTACGCGCAATTTGATTTTGGGTGAGGATCAAGAAACCTGTGACGTGC 417		

OY		478	TGAGCGCCCTCCACCAAGGGCCCATTCGGTCTTCCCCCTTGCGGCCCTCCTCCACAAGAGCAC	477
Db		466	TTCTTCAGACTCTCCACCAGAAGGCCATTCGTCTTCCCCTTGCGAACCCCTCCTCCAAAGAGCAC	525
OY		478	TCTGGAGGCACAGCGCCCTGGCTGCGCTGGTGCACAGAGTAATTCCGCCGAACCGGTGACG	537
Db		526	TTTGGGGGCACAGCGGCC--TGGCGTCTGTGTCAAAGACTAATTCCCGCAACCGGTGACG	583
OY		538	GTCGTGTGGAACCTCAGCGCCCTGTACACAGCGCGTGCACACCTTCGCCGGCTGCTCAG	597
Db		584	GTGTGTGTGAACACTAGCGGCCCTGTACACAGCGCGTGCACACCTTCGCCGGCTGCTCAG	643
OY		598	TCTTAGAGACTTACTCCTCTCAGCAGCGTGTGTGACCGCTGCCCTCCAGACAGCTTG	652
Db		644	TCTCAGAGCTTACTCCTCCTCAGCAGCGTGTGTGACTGTCCCTCCAGCAGCTTG	698
RESULT	10			
LOCUS	Bf663258	983 bp	mRNA	EST
DEFINITION	60214437F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297818 5', mRNA sequence.			21-DEC-2000
ACCESSION	Bf663258			
VERSION	Bf663258.1	GI:11937140		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 983)			
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LILCM1152 row: 1 column: 19 High quality sequence stop: 663. Location/Qualifiers			
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	/clone="IMAGE:4297818"			
	/clone_lid="NIH_MGC_48"			
	/tissue_type="Primary B-cells from tonsils (cell line)"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Organ: B-cells; Vector: pOMB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."			
BASE COUNT	212 a	297 c	296 g	177 t
ORIGIN			1 others	
Query Match	48.5%; Score 364;	DB 151;	Length 983;	
Best Local Similarity	72.1%;	Pred. NO. 2.6e-92;		
Matches	548;	Conservative 0;	Mismatches 195;	Indels 17;
			Gaps 5;	
1 ATGAAGTGGAGCTGGGTTATCTCTTCTCTCTGTCAGTACTACCGCGCTCCATCCCA	60			

Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

Source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADCAXE01"
/clone_1db="ADC"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SODr"
/note="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      140 .a      221 c      172 g      120 t
ORIGIN

```

BASE COUNT	140 a	221 c	172 g	120 t
ORIGIN				

Query Match	48.48;	Score 363;	DB 32;	Length 653;
Best Local Similarity	79.9%;	Pred. No. 4.5e-92;		
Matches 448;	Conservative 0;	Mismatches 95;	Indels 18;	Gaps 1

Db	380	GTGTCATGTGATTTCGCCGACGGGGGGATATTACTTGTGACCACTGGGGGCCAGAAACTCG	439
OY	410	TCACATGCTCGAGGCGCTCCACCAAGGGCCCATCGGCTTCCCTCCGCGCCCTCTCCA	469
Db	440	TCACCGTCTCTAGCCTTCACCAAGGGCCCATCGGCTTCCCTCCGCGCCCTCTCCA	499
OY	470	AGACACCTCTGGGGGACAGACGGCCCTGGGCTGCGGTGTCAGAGACTATTTCCCGAAC	529
Db	500	AGACACCTCTGGGGGACAGACGGG-CCTGGGCTGCCGTGTCAAGAGACTATTTCCCGAAC	558
OY	530	CGGTGACGGGTGTCTGGAACCTCAGGGCCCTGACACAGCGCGGTGCACACCTTCCGGCTG	589
Db	559	CGGTGACGGGTGTCTGGAACCTCAGGGCCCTGACACAGCGCGGTGCACACCTTCCGGCTG	618
OY	590	TCTCAGAGTCTCTGAGACTACTCCCTCAGACGGCGTGGACCGGCCCTCCAGC-AGC	648
Db	619	TCTCAGAGTCTCTGAGACTACTCCCTCAGACGGCGTGGACCGGCCCTTCCAGCAAGT	678
OY	649	TTGGGACCCAGACCTACATCTGCACGTGAATCACAAGCCACGACAA- --CCAAGGTG	705
Db	679	TGGGGACCCAGGACTACATCTGGCACGTGAATCACAAGCCACGACAAACCAACCATGTGG	738
OY	706	GACAGAAAGTTGAGCCCAATCTGTGACAAAACTCACA	745
Db	739	GCCAGAAAGTTGAGCCCAATCTGTGTAAGAACTCACA	778

RESULT 11

LOCUS	AV708715	653 bp	mRNA	EST	09-OCT-2000
DEFINITION	AV708715	ADC Homo sapiens	CDNA clone	ADCAXE01	5', mRNA sequence
ACCESSION	AV708715				
VERSION	AV708715.1	GI:10725980			
KEYWORDS	EST.				
SOURCE	human.				

REFERENCE
AUTHORS

Peng, Y., Song, H.

TITLE
JOURNAL.

COMMENT

Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China

RESULT 12

LOCUS	AM403676	489 bp	EST	16-FEB-2000
DEFINITION	UI-HK-BK0-abh-c-03-0-ui.r1 NIH/MGC_36 Homo sapiens CDNA clone			
ACCESSION	IMAGE:3056237 5', mRNA sequence.			
VERSION	AM403676			
KEYWORDS	AM403676.1	GI:6922685		
SOURCE	EST.			
	human.			

ORGANISM Homo sapiens
 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
 Mammalia: Eutheria: Primates; Catarrhini: Hominoidea; Homo.
 REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 1 (bases 1 to 489)
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: ceqabp-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLMW at:
www-bio.11n1.gov/dbp/1mage/1mage.html
 Seq primer: M13 Forward
 Location/Qualifiers
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 /clone_id="NIH_MGC_36"
 /tissue_type="lymph"
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 /cell_line="MGC85"
 /lab_host="DH10B (LTR)"
 /note="Vector: pT7T3-Pac; Site.1: NotI; Site.2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 116 a 159 c 126 g 88 t
 ORIGIN

Query Match 48.3%; Score 362; DB 115; Length 489;
 Best Local Similarity 85.0%; Pred. No. 8.1e-92;
 Matches 420; Conservative 0; Mismatches 65; Indels 9; Gaps 1;

Oy 252 AGACCGTGTACTATGACGCGTGACACTTTCGACTGATACAGTATACATGAGACTCTCCAG 311
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 5 AGGCGGATTCACCACTCCAGACAGCAATACAGAAACAGCGCTGATCTTCAATGACAG 64
 Oy 312 COTGGATCGGAGGACAGCGCGCTATATTGGCGGCTATTTTGGTTCTACGCC 371
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 65 CCGTAGAGCCGAGGACAGCGCGCTATTACTGTGCGAGAGGAGCGGAGTGGCGATGC 124
 Oy 372 GAATTGTATTATTGATGTTGGGATCAAGAAACCTGTGACACTGTGCGAGCGCTCCAC 431
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 125 -----TTTGTATCTGGGGCCAAAGGACATGTGTACCGCTCTCTACGCTCCAC 175
 Oy 432 CAAGGCGCCATGGCTCTCCCTGGCGCCCTCTCCAAAGACACCTCTGGGGGACAGC 491
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 176 CAAGGCGCCATGGCTCTCCCTGGCACCCCTCCAAAGACACCTCTGGGGGACAGC 235
 Oy 492 GGGCGTGGGTCCTCGTGTCAAGAGATACTTCCCGCAACCGGTGAGGATGTGTGGACATC 551
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 236 AGCCCTGGGTCCTCGTGTCAAGAGATCTTCCCGCAACCGGTGAGGATGTGTGGAAATC 295
 Oy 552 AGGCGCCCTGACACAGGCGGTGCACACCTTCCCGGCTGCTACAGATCTTCAGACTCTA 611
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 296 AGGCGCCCTGACACAGGCGGTGCACACCTTCCCGGCTGCTACAGATCTTCAGACTCTA 355
 Oy 612 CTCCTCTAGACAGCGGTGTGACCGTGCCTCCAGACAGCTTGGGACACCAAGCTACATCG 671
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 356 CTCCTCTAGACAGCGGTGTGACCGTGCCTCCAGACAGCTTGGGACACCAAGCTACATCG 415
 Oy 672 CAAGCTGAATACAAAGCCCGACACACCAAGTGGACAAAGAAAGTTGAGCCCAATCTTG 731
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 Db 416 CAAGCTGAATACAAAGCCCGACACACCAAGTGGACAAAGAAAGTTGAGCCCAATCTTG 475

	732	TGACAAACTCACA	745	OY
Dd	476	TGACAAACTCACA	489	
RESULT	13	Bf663033	936 bp	mRNA
LOCUS	Bf663033	602144936p1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4308537 5'	EST	21-DEC-2000
DEFINITION	mRNA sequence.			
ACCESSION	Bf663033	GI:11936928		
VERSION	EST.			
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	1 (bases 1 to 936)			
TITLE	NIH-MGC http://mhc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	unpublished (1999)			
	Contact: Robert Strusberg, Ph.D.			
	Email: cgabs-remail.nih.gov			
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.			
	cDNA Library Preparation: Ling Hong/Rubin Laboratory			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LMNL at:			
	http://lmnl.lnl.gov			
	Plate: LHCMI180 row: h column: 10			
	High quality sequence stop: 703.			
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	/clone="IMAGE:4308537"			
	/clone_lib="NIH_MGC_48"			
	/tissue_type="Primary B-cells from tonsils (cell line)"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI;			
	Site_2: EcoRI; cDNA made by oligo-dT priming.			
	Directionally cloned into EcoRI/XhoI sites using the			
	following 5' adaptor: GGCACAG(C). Size-selected >500bp			
	for average insert size 1.8kb. Library constructed by Ling			
	Hong in the laboratory of Gerald M. Rubin (University of			
	California, Berkeley) using ZAP-cDNA synthesis kit			
	(Stratagene) and Superscript II RT (Life Technologies).			
	Note: this is a NIH-MGC library."			
BASE COUNT	218 a 279 c 270 g 169 t			
ORIGIN				
Query Match	48.1%	Score 360.8; DB 151; Length 936;		
Best Local Similarity	74.2%; Pred. No. 2.1e-91;			
Matches 524; Conservative	0; Mismatches 172; Indels 10; Gaps 5;			
OY	1	ATGAAGTGAGCTGGGTATTCTCTTCCTCCCTGTAAGTACGCCGGCTCCACTGCCAA	60	
Dd				
	41	ATGAGCATGTGACCTGGAGGGCTCTTCCTGTTGGCTGTAGCTGCAGGTCTCACTCCAG	100	
OY	61	GTCCAACTGGTGCATATCCGCGCCGAGGTCAAGAAGCCAGGCGCTCACTCAAATGTGTC	120	
Dd				
	101	GTGCACAGCTGTGCTAGTCTGGGGCTGAGGTGAGGAAGCCCTGGGGCCCTCAATGAAGTTTCC	160	
OY	121	TGTAAAGCTAGCGGCTATATTTTTCTTCTAATTAATTGGATTCAATGGGTGGCTGAGCCCCC	180	
Dd				
	161	TCCAAGGCGCTTGAGATCACCTTCATCAGGTACTACATCATTCATTTGGGTGCGAAGGCCCT	220	
OY	181	GGGCAAGCGCTTGATGATGTGGGTAGATCTTACCAGCGCTCTGTGTAGCACCAGATATATNC	240	
Dd				
	221	GGACAGAGGCTTGAATACATGATGGCAATAATCAACCTTAGTAGCGGTATGATCAACACTGCA	280	

QY	241	GAATATTTAAAGACCGGTACTACTATGACGGGTACACTTGACATAGTACATATAC	300
Db	281	CAGAA - ATTCCAGGCAGAGTCTTCATGAC - CAGACACGTTAACGAGCACAGTCTACTG	338
QY	301	GAGCTCTCCAGCCTGCATCCGAGGAGACAGCGCGCTCTATTATTCGCGCGTTATTTTTT	360
Db	339	GAGTTTGAGACACCGCTGAGATCTGAGAGACACGGCCGCTGTTATCTGTGCGAGAGCCCGAAGC	398
QY	361	GGTCTAGCCCGAATTGGTATT-----TTGATGTTTGGGGTCAAGGAACCTGTGCTACT	414
Db	399	CAGACGAATTTGTACTACTTTTCCGCAATGGACGCTCTGGGGCCAAAGGACACCGGTACCC	458
QY	415	GTCCTGAGCGCCTCCACCAAGGGCCATCGGTCTTCCCTCTGGGGCCCTCTCCCAAGAGC	474
Db	459	GTCCTCAGCGCTCCACCAAGGGCCATCGGTCTTCCCTCTGGCACCTCTCTCCAAGAGC	518
QY	475	ACCTCTGGGGCACAGGGGCCCTTGGGTGCTGTGTCAAAGCACTACTTCCCGGAACGGGTG	534
Db	519	ACCTCTGGGGCACAGGGGCCCTTGGGTGCTGTGTCAAAGCACTACTTCCCGGAACGGGTG	578
QY	535	ACGGTTCGTGGAACCTCAGGGCGCCCTGACACGAGCGCGACACTTCCCGGCTGTCTTA	594
Db	579	ACGGTTCGTGGAACCTCAGGGCGCCCTGACCAAG - GCGTGGCACACCTTCCCGGTGTCTTAC	637
QY	595	CAGTCTTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGGTGACCGCTCCAGCAGCTTGGGC	654
Db	638	AAGTCTTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGGTGACCGCTCCAGCAGCTTGGGC	697
QY	655	ACCCAGACCTACATCTGAAAGCTGAATTCAAAGCCCAAGCAACACCA 700	
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RESULT 14
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LOCUS
DEFINITION
601811172F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:405414 5',
mRNA sequence.
ACCESSION
BF128792
VERSION
BF128792.1 GI:10967832
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 779)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: LICM893 row: p column: 17
High quality sequence stop: 712.
FEATURES
source
1..779
Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:405414"
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/tissue-type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGC(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling

```

Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

Query Match	48.1%;	Score 360.4;	DB 144;	Length 779;
Best Local Similarity	76.5%;	Pred. No. 2.6e-91;		
Matches 560;	Conservative	0;	Mismatches 156;	Indels 16;
			Gaps	9

QY	21	TCCTTCCTCTCTGCACTAATCTCCGGGCGCACCTCCCAAGTCACTGGTCAATCCGG	80
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QY	81	CGCCGAGTCAAGAGCCAGGGGCTCTAGTCAAAAGTGTCTGTAAAGTACGGCGCTATAT	140
Db	99	GGCTGAGTAGGAGAGGCTGGGGCCCTAGGAGAGGTTTCTCGCAAGGCTCTGGATAC	158
QY	141	TTTTTCTAATTATTGGATTTCATGGGTGGCTCAGGGCCCCGGGCAAGGCTGGAATGGAT	200
Db	159	CTTATCATGGTACTACATTCATTGGGGTGCCAGACGGCCCCCTGGCAAGGGCTTGAATCAT	218
QY	201	GGGAGATCTATCCGGGCTCTGGTAGACCGAATATTACGAAATTTTAAAGACCGTGT	260
Db	219	GGGAAATATATACCTCTAGTAGCGGTAGTCCAAACTACGACAGAA - ATTCCAGGCAAGAT	277
QY	261	TACTATGACGGGTGACACTTTCGACTAGTATACATGATGAGACTCTCCAGCCCTGGCATC	320
Db	278	CTTCATATAC - CAGGACACGTCAACGAGACACAGTCTACATGAGATGAGCAGCCTGATAC	336
QY	321	GGAGGACACGGCGTCTATTTATTTGGCGGCGTTATTTTTTGGTTCAGCCGCAATTTGGTA	380
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QY	381	TT-----TTGATGTTTGGGGTCAAGGACCTTGTCACGTCTCGAGGCCCTCCACCA	434
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QY	435	GGGGCCATCGGTCTTCCCTCGGCGCCCTCTTCCAAGACACTCTGGGGGCAACAGCGGC	494
Db	457	GGGGCCATCGGTCTTCCCTCGGCGCCCTCTTCCAAGACACTCTGGGGGCAACAGCGG -	515
QY	495	CTTGGGCTGCTGTGTCAAGACTACTTCCCCGAAACCGGTGACGSGTGTCTGTGAATCTCAG	554
Db	516	CTTGGGCTGCTGTGTCAAGACTACTTCCCCGAAACCGGTGACGSGTGTCTGTGAAGCTCAG	575
QY	555	CG-CCCTGACAGAGGGGTGACACACTTCCCGGCTCTGCTACAGTCTCTAGAGACTCTACT	613
Db	576	CGCCCCCTGACAGAGGGGTGACACACTTCCCGGCTGTCTACAGTCTCTAGAGACTCTACT	635
QY	614	CCCTCAGCAGCGTGTGACCGGTGCCCTTCAGACGCTTGGGCAACCCAGACTCATCTGCA	673
Db	636	CCCTCAGCAGCGTGTGACCGGTG - CCTCAGCAG - TTGGGCAACCCAGACTCATCTGCA	692
QY	674	ACGTGATTCAGAACCCAGCAACCAAGGTGGACAAGAAAGTTGAGCCCAATCTTGTG	733
Db	693	ACGTGATTCAGAACCCAGCA - CACCAAGGGGGCCAGAAAGTTGAG - CCAATCTTGTG	749
QY	734	ACAAACTCACA 745	
Db	750	AACAAATCACA 761	

RESULT 15				
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	DEFINITION	OV0-HT0366-280100-088-b12	HT0366	Homo sapiens
	ACCESSION	AW606355		CDNA, mRNA sequence
	VERSION	AW606355.1	GI:7311096	
	KEYWORDS	EST.		
	SOURCE	human.		

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 669)

AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QY0642-QY0-HT0366-280100-088-b12&t3=2000-01-28&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 10

Location/Qualifiers

1. 669

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="HT0366"

/dev_stage="Adult"

/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 160 a 191 c 185 g 133 t

ORIGIN

Query Match 47.8%; Score 358.4; DB 118; Length 669;

Best Local Similarity 73.8%; Pred. No. 9,1e-91;

Matches 493; Conservative 0; Mismatches 151; Indels 24; Gaps 2;

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Db 1 GGGGGCGTCCCGGAGATCTCTGTGACAGCTCTGATTTATTTTGTAAATCTAGAT 60

QY 160 CAATGGTGTGCTCAGGCCCCCGGGGCGAGGCTGGAATGGATGGATCTTACCGGC 219

Db 61 GACCTGGGTCCGCAAGGCTCAGGCAAGGGGCTGGAGTGGCCAAATATAGACGAAGAT 120

QY 220 TCTGTACACCGAATATACGGAATTTTAAAGCCGTGTACTATGACGCTGACACT 279

Db 121 GGAACAGACAACTATGTGAGCTGTGGAAGGCCGATTCACCATCTCCAGGACAAAC 180

QY 280 TCGACTAGTACAGTATACATGAGCTCTCAGCTGCGATCGAGAGACAGCGGCTCTAT 339

Db 181 GCCGAGAGTCACTATCTGCAATGACAGCTGAGAGGCGAGACACGGCTGTATAT 240

QY 340 TATTGGCGCG-----TTATTTTGTGTTCTAGCCCGAATTG 377

Db 241 TACTGTGCGAGAAAAAGGTCGATTACGATTTTGAATGGGTATCAAAACAATGA 300

QY 378 GTATTTTATGTGTGGGTCAAGAACCTGTGCTGAGCGCTCCACCAAGG 437

Db 301 TGCTTTTATGTGTGGGCAAGGACAAATGTCATGCTCTTCAGCCTCCACCAAGG 360

QY 438 CCCATCGGCTTCCCGTGGGCGCTCTCCAAAGACACCTGGGGGCGACAGCGGCCCT 497

Db 361 CCATTCGGTCTTCCCGTGGGCAAGCTCTCCAAAGACACCTGTGGGGCGACAGCGGCCCT 420

QY 498 GGGCTGCTGTCAAGGACTATTCGCAACGGTGAAGGTGTGGAACCTCAGGCGC 557

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Search completed: July 20, 2001, 01:57:51

Job time: 4179 sec

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QY 558 CTTGACCGGCGGTGCAACACTTCCGGGTGCTTACAGTCTCAGAGACTCTACTCCT 617

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QY 618 CAGCAGGTGTGACGCTGCTCCACAGCTTGGGACCCAGACCTTACATCTGCAAGT 677

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QY 678 GAATCAACAGCCCAAGCAACCAAGTGTGACCAAGATTGAGCCCAATCTGTGACAA 737

Db 601 GAATCAACAGCCCAAGCAACCAAGTGTGACCAAGATTGAGCCCAATCTGTGACAA 658

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Db 659 AATCAACA 666

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 02:38:19 ; Search time 181.81 Seconds
(without alignments)
2590.211 Million cell updates/sec

Title: US-08-487-283a-12

Perfect score: 750
Sequence: 1 ATGAGTGGAGCTGGTTAT.....GTGACAAACTCACATTA 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750	100.0	750	16 AAT08484	Humanised 5G1.1 VH
2	737.2	98.3	750	16 AAT08487	Humanised 5G1.1 VH
3	729.2	97.2	750	16 AAT08483	Humanised 5G1.1 VH
4	561.2	74.8	750	16 AAT08482	Chimeric heavy Cha
5	505.2	67.4	2077	21 AAA11655	Humanised anti-Fas
6	495.2	66.0	8119	20 AA90575	Plasmid p6G4V1IN35
7	495.2	66.0	8119	21 AA287975	Nucleotide sequenc
8	495.2	66.0	8120	21 AAC65515	Humanised anti-IL-
9	494	65.9	2071	19 AA90080	Anti-Fas humanised
10	494	65.9	2071	21 AAA72184	DNA encoding human
11	494	65.9	2071	21 AAA11622	Humanised HFE7A de

12	492.4	65.7	2073	21 AAA11646	Humanised anti-Fas
13	490.8	65.4	2073	21 AAA11644	Humanised anti-Fas
14	490.8	65.4	2073	21 AAA11645	Humanised anti-Fas
15	490.4	65.4	8120	19 AA94956	Anti-IL-8 humanise
16	489.2	65.2	2077	19 AA90079	Anti-Fas humanised
17	489.2	65.2	2077	21 AA72159	DNA encoding human
18	489.2	65.2	2077	21 AAA11597	Humanised HFE7A de
19	488	65.1	799	21 AA287976	Humanised anti-IL-
20	488	65.1	800	20 AA90582	6G4V1IN35A Fab' he
21	488	65.1	800	21 AAC65516	Humanised anti-IL-
22	488	65.1	801	19 AA955073	Humanised anti-IL-
23	488	65.1	927	19 AA955072	Humanised anti-IL-
24	488	65.1	927	20 AA90578	Humanised anti-IL-
25	488	65.1	927	21 AAC65508	Anti-IL-8 6G4-2-5V
26	488	65.1	927	21 AA287969	Humanised anti-IL-
27	488	65.1	6563	19 AA94953	Anti-IL-8 humanise
28	488	65.1	6563	20 AA90579	p6G4V1IN35A.F(ab') Anti-IL-8 6G4-2-5V
29	488	65.1	6563	21 AAC65509	Nucleotide sequenc
30	488	65.1	6563	21 AA287970	Monoclonal antibod
31	487.8	65.0	1449	20 AA906951	Monoclonal antibod
32	487.8	65.0	1449	20 AA906952	Humanised 323/A3 (
33	487.8	64.4	1418	22 AA963374	DNA encoding a dim
34	479.2	63.9	1413	21 AA963531	Antibody D heavy c
35	478.2	63.8	1617	14 AA035089	Vector contg. TCAR
36	476	63.5	9208	15 AA065629	Target plasmid Mol
37	476	63.5	19001	19 AA961793	VEGF humanised ant
38	472.8	62.8	6072	19 AA971266	Fab-display antibod
39	471.2	62.8	6072	19 AA963493	DNA encoding VH re
40	467.4	62.3	3282	17 AA940914	Modified heavy cha
41	467.4	62.3	3282	21 AAA31024	B12 Iggl sequenc
42	467.4	62.3	3282	21 AAA32164	Nucleotide sequenc
43	467.4	62.3	13254	17 AA940915	pEel2 Combo BM 12
44	467.4	62.3	13254	21 AAA31025	pEel2 Combo BM 12
45	467.4	62.3	13254	21 AAA32151	

ALIGNMENTS

RESULT 1	
ID AAT08484	standard; DNA; 750 BP.
XX	
AC AAT08484:	
XX	
DT 02-APR-1996	(first entry)
XX	
DE Humanised 5G1.1 VH + IGHRLC DNA.	
XX	
KM Complement C5; haemolysis; kidney; glomerulonephritis;	
KW monoclonal antibody; anti-inflammatory; antibody engineering;	
KW humanised antibody; complementarily determining region; CDR;	
KM ds.	
XX	
OS Synthetic.	
XX	
FH Key	Location/Qualifiers
FT CDS	1..750
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FT sig_peptide	1..57
FT	/**tag- b
FT mat_peptide	58..747
FT	/**tag- c
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PN W09529697-A1.	
XX	
PD 09-NOV-1995.	
XX	
PE 01-MAY-1995;	95WO-US05688.
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PR 02-MAY-1994;	94US-0236208.
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PA (ALEX-) ALEXION PHARM INC.	

Query Match	Best Local Similarity	100.0%	Score 750;	DB 16;	Length 750;
Matches 750;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
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Db 1 atgaagtggagctgggtatctctctctccctgcagtaactgcggtccactcccaa 60					
OY 61 GTTCAACGTGTCATTCGGCGCGAGGTCAAGAGCCGAGGGGCTTCATCAAGTGTCC 120					
Db 61 gtcccaactggtgcaatccgcgcgcgaggaagcaagcgagcgccacgtaagaatgtcc 120					
OY 121 TGTAAAGCTAGGGGCTATTATTTTCTTAATATATATGATTAATGAGTCAATGGGTGCGTACGGCCCC 180					
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Db 361 ggtctagcccgaaattgttatattgattggttggttcaaggaacctgttcaactgtctcg 420					
OY 421 AGCGCTTCACCAAGAGGCGCATGGGTCTTCCCGTGGGGCTCCTCTCCAAAGACACTCT 480					
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Db 481 gggggcacaagcgccctggtgctgtgtcgtgtcgaagactatctcccgaaacggtgaagtg 540					
OY 541 TCGTGGAACCTAGGCGCCTTGACACAGCGGCTGACACACTTCCGGCTGTCTACAGTCC 600					
Db 541 tcgtggaactcaagcgccctgacacagcggtgtgacacacttccggctgtctctacagttcc 600					
OY 601 TCAGGACCTTACTCCCTTCAGCAGCGTGGTGAACCTGTGCGCTCCAGCAGCTTGGGACCCAG 660					
Db 601 ttcaggaccttactcccttccagcagcggtggtagacgtgtgcccctccagcagcttgggacccag 660					

Query Match	98.3%	Score 737.2	DB 16	Length 750
Db	601	tcagaccctactccctcagaagcgttgtagccgtgcctccctccagcagcttgggcaccag	660	
Oy	661	ACCTACATCTGCAACGTGATACACAGCCAGCAACCAAGTGGACAAAGATTGAG	720	
Db	661	acctacatctgcgaactgtaacacaaagccgacaaacccaagctggaagaagttag	720	
Oy	721	CCCAATCTGTGAGCAAAACACACACATTA	750	
Db	721	cccaatcttctgacaaactcacataa	750	
RESULT 2				
AA08487				
ID	AA08487	standard; DNA, 750 BP.		
XX				
AC	AA08487			
XX				
DT	02-APR-1996	(first entry)		
XX				
DE	Humanised 5G1.1 VH + IGHRLD DNA.			
XX				
KW	Complement C5; haemolysis; kidney; glomerulonephritis;			
KW	monoclonal antibody; antiinflammatory; antibody engineering;			
KW	humanised antibody; complementarity determining region; CDR;			
KM	ds.			
XX				
OS	Synthetic.			
XX				
FH	Key	Location/Qualifiers		
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FT		/*tag= c		
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PD	09-NOV-1995.			
XX				
PE	01-MAY-1995;	95WO-US05688.		
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PR.	02-MAY-1994;	94US-0236208.		
XX				
PA	(ALEX-) ALEXION PHARM INC.			
PI	Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;			
PI	Rocher RP, Springhorn J F, Squinto SP, Thomas TC;			
PI	Wang Y, Wilkins JA;			
XX				
XX	WPI; 1995-392923/50.			
DR	P-PSDB; AAR77615.			
XX				
PT	Treating glomerulonephritis with antibody against complement C5			
PT	component - to inhibit complement induced cell lysis			
PS	Claim 37; Pages 135-137; 181pp; English.			
XX				
CC	A DNA construct (AA08487) codes for a humanised CDR-grafted			
CC	light chain, designated 5G1.1 VL + IGHRLD (AAR77615), which includes			
CC	CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The			
CC	DNA can be subcloned together with DNA (AA08484) coding			
CC	for a humanised Fd (AAR77611) into vector APEX-3P (AA08476) for			
CC	expression of humanised antibody in human 293 EBNA cells. Such			
CC	recombinant antibodies retain the ability of Mab 5G1.1 to block			
CC	human complement C5a generation and thus to reduce glomerular			
CC	inflammation and kidney dysfunction associated with			
CC	glomerulonephritis.			
XX				
Sequence	750 BP; 160 A; 223 C; 198 G; 169 T; 0 other;			

Best Local Similarity 98.9%; Pred. No. 2,4e-168;
Matches 742; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

OY 1 ATGAAGTGGAGCTGGGTATTTCTTCCTCTGTCAGTAAGTCCGGCGCTCCAA 60
Db 1 atgaagtggagctgggtatttcttctcctctgtaactcgcgcactccaa 60
OY 61 GTCCAACTGTCGAATCCGGCGCGAGGTCAGAACCCAGGGCTTCAGTCAAGTCC 120
Db 61 gtccaaactgtcgaaatccggcgaggaagccaggggcctcagcaagtgcc 120
OY 121 TGTAAAGCTAGGCGGTATTTTCTAATTTATGATTCATGGGCGCTCAGGGCCCC 180
Db 121 tgaagctagcggtatcttctcaatcaltgatacagggcgccagggcccc 180
OY 181 GGGCAGGGCGCTGGAATGATGGGTGAGATCTTACCGGGCTGTGTGACACGAATATAC 240
Db 181 gggcagggcgtggaatgatgggtgagatcttacgggctgtgtgacacgaatatacc 240
OY 241 GAAATTTTAAAGACCGTGTACTATGACGCGGTGACACTTGCATAGTACATACATG 300
Db 241 caaaatttcagagcggtgtactatgactctgacactcagctagatacatag 300
OY 301 GAGCTCTCAGCGCTGATGAGGAGGAGGAGCGGCTATATGCGGCGCTATTTT 360
Db 301 gagctctcagcgctgatgaggaggagcgccgctatatactgcgcgtacttctt 360
OY 361 GGTCTAGCGCCGAATTTGATTTTGTGTTGGGTGCAAGAACCCGTGCTGCTCG 420
Db 361 ggtctagcgccgaatttgatttggttgggtgcaagaacccgtgctgctctcg 420
OY 421 AGCGCTCCACCAAGGCGCCATGCTTCCTCCGCGCTCTCTCAAGACACTCT 480
Db 421 agcgctccaccaagggcccatcgctctcccgctgcgccctctcaagacactct 480
OY 481 GGGGCGACAGCGCCCTGGGCTGCTGTCGAAGACTACTTCCCGACCGGTGACGCTG 540
Db 481 ggggcgacagcgccctgggctgctgtcgaagactacttcccgacccggtgacgctg 540
OY 541 TCGTGGAACTAGGCGCGCTGACACGCGGCTGACACTTCCCGGCTGCTCTACAGTCC 600
Db 541 tcgtggaaactagcgcgctgacacgcggtgacacacttcccgctgctctacagttcc 600
OY 601 TCAGACTCTACTCCTCTGACAGCGGTGTGACCGTCCCTCAAGCACTTGCGACCCAG 660
Db 601 tcagactctactcctctgacagcggtgtgacccgtgcccccaagccttggtgacccag 660
OY 661 ACCTACATCTGCAACGTGAATCAAGCCGACGACCAAGAGTGGCAAGAAATTGAG 720
Db 661 acctacatctgcaacgtgaatcaagccgacgacacacaaagtgcaagaagttag 720
OY 721 CCCAATCTTGTGACAAAACCTCAACATTA 750
Db 721 cccaatcttgtgacaaaactcaacataa 750

```

RESULT 3
AAT08483
ID AAT08483 standard: DNA, 750 BP.

AA08483;
15-MAR-1996 (first entry)
Humanised 5G1.1 VH + IGHRL DNA.
Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
ds.
Synthetic.

```

FH Key Location/Qualifiers
FT CDS 1..750
FT sig_peptide /tag= a
FT /tag= 1..57
FT /tag= b
FT mat_peptide 58..747
FT /tag= c
PN W09529697-A1.
PD 09-NOV-1995.
PE 01-MAY-1995; 95WO-US05688.
PR 02-MAY-1994; 94US-0236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Mattis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
DR WPI: 1995-392923/50.
DR P-PSDB: AAR77610.
XX
XX
XX Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS
XX Claim 42; Page 119-122; 181pp; English.
XX
XX A DNA construct (AAT08483) codes for a humanised CDR-grafted and
CC framework sequence-altered Fd 5G1.1 VH + IGHRL (AAR77610), which
CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
CC The DNA can be subcloned together with DNA (AAT08484) coding for a
CC humanised light chain (AAR77612) into vector APEX-3P (AAT08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of MAb 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
XX
SQ Sequence 750 BP; 159 A; 225 C; 199 G; 167 T; 0 other;

Query Match 97.2%; Score 729.2; DB 16; Length 750;
Best Local Similarity 98.3%; Pred. No. 2e-166;
Matches 737; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 ATGAAGTGGAGCTGGGTATTTCTTCCTCTGTCAGTAAGTCCGGCGCTCCAA 60
Db 1 atgaagtggagctgggtatttcttctcctctgtaactcgcgcactccaa 60
OY 61 GTCCAACTGTCGAATCCGGCGCGAGGTCAGAACCCAGGGCTTCAGTCAAGTCC 120
Db 61 gtccaaactgtcgaaatccggcgaggaagccaggggcctcagcaagtgcc 120
OY 121 TGTAAAGCTAGGCGGTATTTTCTAATTTATGATTCATGGGCGCTCAGGGCCCC 180
Db 121 tgaagctagcggtatcttctcaatcaltgatacagggcgccagggcccc 180
OY 181 GGGCAGGGCGCTGGAATGATGGGTGAGATCTTACCGGGCTGTGTGACACGAATATAC 240
Db 181 gggcagggcgtggaatgatgggtgagatcttacgggctgtgtgacacgaatatacc 240
OY 241 GAAATTTTAAAGACCGTGTACTATGACGCGGTGACACTTGCATAGTACATACATG 300
Db 241 caaaatttcagagcggtgtactatgactctgacactcagctagatacatag 300
OY 301 GAGCTCTCAGCGCTGATGAGGAGGAGGAGCGGCTATATGCGGCGCTATTTT 360
Db 301 gagctctcagcgctgatgaggaggagcgccgctatatactgagcggtacttctt 360
OY 361 GGTCTAGCGCCGAATTTGATTTTGTGTTGGGTGCAAGAACCCGTGCTGCTCG 420

```



```

QY 421 AGCCCTCCACCAAGGCCATCGGTCTCCCTCGCGCCCTCTCCAGAGCACCTCT 480
    |||||||
Db 1726 tcggccctccaccaaggcccatcggtctccctccctgcacacctctccaagagcaacctct 1785
QY 481 GGGGGCAGCGGGCCCTGGCTGCTGTCAGAGACTACTTCCCGAAGCCGCTGACGGTG 540
    |||||||
Db 1786 gggggcacaaggccctgggtgctgctgcaagagactacttcccgaaacggtgacggtg 1845
QY 541 TCCTGGAAGTACAGCGCCCTGACAGCGCGCTGACACCTTCCCGGCTGTCTACAGTCC 600
    |||||||
Db 1846 tcggtggaactcaggcgccctcagcagcggtgcaacaccttccggtcgtctcaagttcc 1905
QY 601 TCAGGACTCTACTCTCCAGCAGCGGTGTGACCGTCCCTCCAGCAGCTTGGGCAACCCAG 660
    |||||||
Db 1906 tcagagactctactccctcagcagcggtgtgactgtgacctcagcagcttgggcaaccag 1965
QY 661 ACCATCATCTGCAACGTAAATCACAAGCCCGACAAACACCAAGGTGACAAAGTGTGAG 720
    |||||||
Db 1966 acctacatctgcaacgltgaatcacaaagcccgcaaccacaagtgtagacaagaagttag 2025
QY 721 CCCAATCTTGTGACAAAACTCACACAT 748
    |||||||
Db 2026 cccaatctgtgacaaaactcacacat 2053

RESULT 9
AAV70080
ID AAV70080 standard; DNA; 2071 BP.
XX
AC AAV70080;
XX
DX 15-MAR-1999 (first entry)
DE Anti-Fas humanised antibody HFE7A heavy chain DNA.
XX
KM HFE7A, monoclonal antibody; mouse: Fas; humanised antibody;
KM apoptosis; HFE7A: autoimmune disease; Hashimoto's disease;
KM systemic lupus erythematosus; graft versus host disease;
KM Sjogren syndrome; pernicious anaemia; Addison's disease;
KM scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KM rheumatoid arthritis; autoimmune haemolytic anaemia;
KM masthenia gravis; multiple sclerosis; Basedow's disease;
KM thrombopenia purpura; insulin-dependent diabetes; allergy;
KM atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KM glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KM transplant rejection; therapy; ds.
XX
OS Homo sapiens.
OS Synthetic.
FH Key CDS
FT 21..2039 location/Qualifiers
FT /*tag= a
FT /note= "contains introns"
FT 21..77
FT /*tag= b
FT 1..735
FT /*tag= c
FT /number= 1
FT /codon_start= 21
FT 736..1126
FT /*tag= d
FT /number= 1
FT 1127..1171
FT /number= 1
FT /*tag= e
FT /number= 2
FT 1172..1289
FT /*tag= f
FT /number= 2
FT 1290..1619
FT /*tag= g
FT /number= 3
FT 1620..1716
FT Intron
FT Intron

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FT /*tag= h
FT /number= 3
FT 1717..2071
FT /*tag= 1
FT /number= 4
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PN AU9859701-A.
XX
PD 08-OCT-1998.
XX
PF 30-MAR-1998; 98AU-0059701.
XX
PR 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX
PA (SANTY ) SANKYO CO LTD.
PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
DR MPI: 1998-543440/47.
DR P-PSDB; AAW83037.
XX
PS Claim 27; Page 223-225; 292pp; English.
XX
CC This nucleotide sequence codes for the HV type humanised heavy
CC chain (see AAW83037) of murine anti-human Fas monoclonal antibody
CC HFE7A. It was prepared from plasmid pGHS17A62 (see AAV70079) by
CC PCR amplification (see AAV70115-17), and includes humanising R44G
CC and A76T amino acid substitutions. Host cell Escherichia coli
CC pGHPDHV3 SANK 70298 harbors plasmid pGHPDHV3 carrying a fusion
CC fragment of the humanised HV type HFE7A heavy chain and DNA
CC encoding human IgG1 constant region, and is deposited as
CC FERM BP-6273 (claimed). The invention provides methods for
CC producing humanised antibodies by culturing host cells. Humanised
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
CC of inducing apoptosis in abnormal cells expressing Fas, and of
CC inhibiting Fas-induced apoptosis in normal cells. The humanised
CC antibodies are used to evaluate, in animal models, treatments of
CC diseases that involve Fas/Fas ligand interactions, and also to
CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple sclerostis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

Query Match 65.9%; Score 494; DB 19; Length 2071;
Best local Similarity 81.5%; Pred. No. 8,7e-110;
Matches 585; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

QY 1 ATGAAGTGAAGCTGGGTTATCTCTCTCTCTGTCAGTAACAGCGGCTCCACCTCCAA 60
    ||| ||||||| ||| ||||||| ||| ||| ||| ||||||| |||
Db 21 atggatgagcgctgatacctctctcttgtagcaacagctacagtgctccactcag 80
QY 61 GTCCAACTGCTGCAATCCGCGCGCGAGGTCAGAGCAAGCGGCTCTAGTCAAGTCTCC 120
    ||||||| ||||||| ||| ||| ||||||| ||||||| ||| ||| ||| |||
Db 81 gtccaactggtgagctcgtgagctgagtcagaagacgcttgcagtgagtgatctc 140
QY 121 TGTAAAGCTAGCGGCTATATTTTTCATTTATTTGATTTCAATGGGTCGTCAGGCCCC 180
    || || ||| ||||| || || || || ||||| || ||||| |||||||

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Db 141 tgcgaagcttcggtcgaacccctaccagctactgtagtcagtgaggtgaaacagggccct 200
 Oy 181 GGGCAGGCGCTGGAAATGATGGGTGAGATCTTACCGGGCTGTGTAGCACCGAATATACC 240
 Db 201 ggcacagggccttgagtgatggagatgatgacccctctgatactataactataacat 260
 Oy 241 GAAAAATTTAAAGACCGGTGTACTATGACCGGTGACACTTCCGCTAGTACATATACATG 300
 Db 261 caaaagttcaagggcgaagccacatgtagtgcacacatccactagcacagcctacatg 320
 Oy 301 GAGCTCTCAGCGTGGATGGAGGAGACAGCGCGCTGATATATATGCGGGCTTTATTTT 360
 Db 321 ggcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 377
 Oy 361 GGTCTTAGCCCAATTTGATTTTGTGTTGGGTCAAGGAACCGTGTACATGCTGC 420
 Db 378 gactatagtaaacacactgactcgtatgctggtggaagagacccctgacacgctctcc 437
 Oy 421 AGCGCTCCACCAAGGGCCCATGCTTCCTCCCTGGCGCTCTCCACAGACACCTCT 480
 Db 438 tcagcctccacacagggccatcgtctccctctgacacccctccacagagacacct 497
 Oy 481 GGGGACAGCGCGCTGGCTGCTGCTGCTCAAGGACACTTCCCGAAGCGGTGAGCGTG 540
 Db 498 gggggacagcagcgccctgagcagcagcagcagcagcagcagcagcagcagcagcag 557
 Oy 541 TCGTGGAACCTCAGGCGCGCTGACAGCGCGGTGACACCTTCCCGCTGTCTACATGCC 600
 Db 558 tcgtggaactcagcgccctgacacagcggtgacacacccctcccgctgtctacacgtcc 617
 Oy 601 TCAGACTCTACTCCTCAGACAGCGGTGTGACCGCTCCACAGACCTTGGGACCCAG 660
 Db 618 tcaggaactcactccctcagcagcggtgacacgctccctcagcagcagcagcagcagcag 677
 Oy 661 ACCTACATCTGCAAGTGATCAGACAGCGCGGTGACACCGAGGTGAGCAAGATTG 718
 Db 678 acctacatctgcaagcgtgatacacaagccagacaacaaagtgagacaagagatg 735

RESULT 10
 AAA72184
 ID AAA72184 standard: DNA; 2071 BP.

AC AAA72184;
 XX
 DE 24-NOV-2000 (first entry)
 XX
 DE DNA encoding humanised anti-Fas antibody heavy chain, SEQ ID NO:116.
 XX
 KM Anti-Fas antibody; monoclonal antibody HFE7A; PERM-BP-5828;
 KM murine; humanised antibody; complementarity determining region: CDR;
 KM human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KM autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KM cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KM hepatitis; AIDS; graft rejection; heavy chain: ds.
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 PD 20-JUN-2000.
 XX
 PE 30-SEP-1999; 99JP-0278301.
 PR 30-SEP-1998; 98JP-0276883.
 PA (SANKY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR P-PSDB: AAB14779.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality

PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX
 PS Example 22; Page 106-108; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention of treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine-anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAA72146, AAA72159 and AAA72184
 CC represent DNA encoding the heavy chains (or fragments thereof) of
 CC various humanised HFE7A-derived anti-Fas antibodies.
 XX
 SQ Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

Query Match 65.9%; Score 494; DB 21; Length 2071;
 Best Local Similarity 81.5%; Pred. No. 8.7e-110;
 Matches 585; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

Oy 1 ATGAAGTGAGACTGGGTATTTCTCTCTCTGATGAATGAGCGCGGCTCAGTCCAA 60
 Db 21 atggatggagctgatalcatcctctcttgtagaacaagctacagtgctcactctag 80
 Oy 61 GTCCAACTGTGTCAATCCGCGCGAGGTCAAGAACCGAGGCGCTCAGTCAAGTGTCC 120
 Db 81 gtccaactggtgactctggtggtcgaagagccttggtcagtgaaagtgtcc 140
 Oy 121 TGTAAAGCTACGCGCTATATTTTCTATTTTGGATTTCAATGGGTGCGTACGCGCC 180
 Db 141 tgcgaagcttcgtctacacccacagcagcagcagcagcagcagcagcagcagcagc 200
 Oy 181 GGGGAGGCGCTGGAATGATGGGTGATCTTACCGGCTCTGAGACCGCAATATACC 240
 Db 201 ggcacagggccttgatgagtgatgagatgatactctctgtagatactataactataacat 260
 Oy 241 GAAAAATTTAAAGACCGGTGTACTATGACCGGTGACACTTCCGCTAGTACATATACATG 300
 Db 261 caaaagttcaagggcgaagccacatgtagtgcacacatccactagcacagcctacatg 320
 Oy 301 GAGCTCTCAGCGTGGATGGAGGAGACAGCGCGGTGATATATATGCGGGCTTTATTTT 360
 Db 321 gactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 377
 Oy 361 GGTCTTAGCCCAATTTGATTTTGTGTTGGGTCAAGGAACCGTGTACATGCTGC 420
 Db 378 gactatagtaaacacactgactcgtatgctggtggaagagacccctgacacgctctcc 437
 Oy 421 AGCGCTCCACCAAGGGCCCATGCTTCCTCCCTGGCGCTCTCCACAGACACCTCT 480
 Db 438 tcagcctccacacagggccatcgtctccctctgacacccctccacagagacacct 497
 Oy 481 GGGGACAGCGCGCTGGCTGCTGCTGCTCAAGGACACTTCCCGAAGCGGTGAGCGTG 540
 Db 498 gggggacagcagcgccctgagcagcagcagcagcagcagcagcagcagcagcagcag 557
 Oy 541 TCGTGGAACCTCAGGCGCGCTGACAGCGCGGTGACACCTTCCCGCTGTCTACATGCC 600
 Db 558 tcgtggaactcagcgccctgacacagcggtgacacacccctcccgctgtctacacgtcc 617
 Oy 601 TCAGACTCTACTCCTCAGACAGCGGTGTGACCGCTCCACAGACCTTGGGACCCAG 660
 Db 618 tcaggaactcactccctcagcagcggtgacacgctccctcagcagcagcagcagcagcag 677
 Oy 661 ACCTACATCTGCAAGTGATCAGACAGCGCGGTGACACCGAGGTGAGCAAGATTG 718

KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI: 2000-258930/23.
 DR P-PSDB; AAM90935.
 PT
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Claim 35; Page 177-180; 263pp; English.
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence encodes
 CC a humanised anti-Fas antibody heavy chain construct designated Hen 3
 CC which is described in the method of the invention.
 CC
 CC
 XX
 SQ Sequence 2073 BP; 461 A; 686 C; 559 G; 367 T; 0 other;

Query Match 65.7%; Score 492.4; DB 21; Length 2073;
 Best Local Similarity 81.3%; Pred. No. 2.1e-109;
 Matches 584; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

QY 1 ATGAAGTGGAGCTGGGTATTCTCTTCCTCCCTGTCAGTACTCCGCGCTCCACTCCCA 60
 DB 23 atggaatgagctgtatctctctctctctgttgcacacgtacaggtgtccattctcag 82
 QY 61 GTCCAAATGCTCAATCCGCGCGCGGCGGTCAGAACGCCAGGGGCTCAGTCAAAAGTCTC 120

Db 83 gtccaaactggcgcgctctggtgcctgaagtcagaagccctgggcttcagtgaaagtctc 142
 QY 121 TGTAAAGCTAGCGGCTATATTTTCTTAATTTATTTGATTCATAGTGCCTCAGGCCCC 180
 Db 143 tgcgaagctcttgctacacacttaccacagctcagtgatgcagtggtacgcagccct 202
 QY 181 GGGCAGGCGCTGGAATGATGGTGAGATCTTACCGGGGCTTGCTGACCGCAATATACC 240
 Db 203 ggaacaagctatgtatgtgagatltgatctctctctgtagctataactataat 262
 QY 241 GAAATTTTAAAGCCGTATTACTATGACGCGTACACCTTGACAGTACAGTATACATG 300
 Db 263 caaaglttcaagggcagaatcactgactgtagacacactcactacagcctacatg 322
 QY 301 GAGCTTCACAGCCGTCGATCGAGACAGGCGCTCTATTATTTGCGGCGCTTATTTT 360
 Db 323 gactcagcagcctgagatctgagacacagcggtctatctatctgtgcaagaa---tag 379
 QY 361 GATTCTAGCCCGAATGTGATTTGATGTGGGTCAGGAACCCCTGCTACTGCTCG 420
 Db 380 gactatgatacaactgtacttgatctgctgtgggccaagttacactgtccacgtctcc 439
 QY 421 AGCGCTCCACACAGGCGCCATCGGTCTTCCCTGGCGCCCTCTCCAAAGACCTCT 480
 Db 440 tcaagctccaccaaaggccactgctctcccttgacacctctccaagacactct 499
 QY 481 GGGGCGACAGCGCGCGCTGCGTGGTCAAGACACTTCCCGAACCGTACAGGTG 540
 Db 500 ggggacacagcgccctgggtgctgctgtaagaactacttcccgaaacggtgacgtg 559
 QY 541 TCGTGAACCTCAGGCGCCCTGACAGCGGCGGTGACACACTTCCGCGTCTACACTC 600
 Db 560 tctggaactcgaagcgccctgacacagcggtgacacaccttcccggtctctcaagttcc 619
 QY 601 TCAGACTCTACTCTCCCTCAGACGCTGTGACGCTGCCCTCCACAGCTTGGACCCAG 660
 Db 620 tcaagactctactctccctcagcagtggtgacgctgctcccaagaagttggaaccag 679
 QY 661 ACCACATCTGCAACGTAATCACAAGCCGACCAACCAAGGTGACCAAGATTTG 718
 Db 680 acctacatctgcaagcgtgaatcacaagcccgcaacacgaagtggaagaagtggtg 737
 RESULT 13
 ID AAA11644 standard; DNA: 2073 BP.
 AC AAA11644;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas designed heavy chain Hen 1 DNA.
 XX
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX (SANY) SANKYO CO LTD.
XX Serizawa N, Hanyama H, Nakahara K, Tamaki I, Takahashi T;
PI WPI: 2000-258930/23.
DR P-PSDB; AAW90933.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Claim 33; Page 166-168; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antineumatic, nephroprotective, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (II) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence encodes
CC a humanised anti-Fas antibody heavy chain construct designated Heu 1
CC which is described in the method of the invention.
XX
SQ Sequence 2073 BP; 462 A; 685 C; 559 G; 367 T; 0 other;

Query Match 65.4%; Score 490.8; DB 21; Length 2073;
Best Local Similarity 81.2%; Pred. No. 5.1e-109;
Matches 583; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

QY 1 ATGAAGTGAAGCTGGGTTATCTTCTCTCTGTCAGTAATGCGGCGTCACATCCCAA 60
DB 23 atggagtgagagctatcatctctctcttgtagcaacagctacagtgctcatctcag 82
QY 61 GTCCAACTGGTGCATCGGCGCGGAGTCAAGAACCCAGGCGCTCGTCAAAATGTCC 120
DB 83 gtccaactggtgcagctctgtaggagtcagaagagcttgcagtgtaaggtgtccc 142
QY 121 TGTAAAGCTAGCGGCTATATTTTCTAATTTATGATTCATAGGGTGCCTCAGGCCCC 180
DB 143 tgcaggctcttgctacaccttcaccagctacgtatgagtgtaaaacaggccct 202
QY 181 GGGCAGGCGCTGGAATGAGATGGGAGATCTTACCGGCGCTGTGGTAGCAGCAATATACC 240
DB 203 ggcacaggaacttgatgtagagagatgatcctcttcgtatgatacctaacaacat 262
QY 241 GAAATTTTAAAGACCTGTTACTAGACCGCGTGCACCTAGTACAGTATATATG 300
DB 263 caaaagtccaaggaagcaccacatgactgtatgacacatccacagcagccacatg 322
QY 301 GAGCTCTCAGCCTGCGATCGAGACAGCGCCGTATATTATGCGCGCTTATTTT 360

DB 323 gagctcagcagcctgagatctggagacagcgctctattactgtgcaagaa---tagg 379
QY 361 GGTTCAGCCCCGAATGTGATTTGTGTTGGGTCAGAGAACCTGTGCATGTCCTG 420
DB 380 gactatagtaaaacagctactcagatgtctgggccaaggtacactgtctaccgtctcc 439
QY 421 AGCGCTTCACCAAGGGCCATGCGTTCCTCCCTGGCGCCCTCTCCAAAGACACTCT 480
DB 440 taagctccaccaagggcccatctgctctcccttgacacctctcccaagagacctct 499
QY 481 GGGGACAGACGGCCCTGGGCTGCTGTCAGAGACTACTTCCCGACCGGTGACGCTG 540
DB 500 ggaggacagcgcccttggtgctgctgcaagactactctcccgacagcgagcggtg 559
QY 541 TCGTGAATCTAGCGGCCCTCGACACCGCGCTGACACCTTCCCGGCTGCTCAGACTC 600
DB 560 tctgtgaactcagcgcccttgaccagcggtgacacactctccgctgtctctacagctc 619
QY 601 TCAGACCTTACTCCCTCAGACGCTGTGACCGTCCCTCCAGAGCTTGGGACCCAG 660
DB 620 tcagagacttactcctctcagcggtgtgagccgtgtcctccagcgcttggtgacccgg 679
QY 661 ACCTACATCTGCAACGTGAATCACAAGCCCGACAGACCAAGGTGACAGAAAGTTG 718
DB 680 acctacatctgcagctgagatcacagccacagacacacaaagtgagcaagagatgtg 737

RESULT 14
AA11645
ID AA11645 standard; DNA; 2073 BP.
AC AA11645;
XX 08-AUG-2000 (first entry)
DE Humanised anti-Fas designed heavy chain Heu 2 DNA.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatologic; immunosuppressive; thyromimetic; antineumatic; anti-Fas;
KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
OS Synthetic.
XX
PN EP990663-A2.
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
XX (SANY) SANKYO CO LTD.
PI Serizawa N, Hanyama H, Nakahara K, Tamaki I, Takahashi T;
DR WPI: 2000-258930/23.
DR P-PSDB; AAW90934.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Claim 34; Page 172-174; 263pp; English.

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 02:35:04 ; Search time 86.76 Seconds
(without alignments)
1636.507 Million cell updates/sec

Title: US-08-487-283A-12

Sequence: 1 ATGACGTGAGCTGGCTTAT.....GTGACAAACTCACACATAA 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495.2	66.0	8120	3	US-09-027-449-68
2	495.2	66.0	8120	3	US-09-026-985-68
3	488	65.1	800	3	US-09-027-449-69
4	488	65.1	800	3	US-09-026-985-69
5	488	65.1	927	3	US-09-027-449-59
6	488	65.1	927	3	US-08-804-444A-59
7	488	65.1	927	3	US-09-026-985-59
8	488	65.1	6563	3	US-09-027-449-61
9	488	65.1	6563	3	US-08-804-444A-61
10	488	65.1	6563	3	US-09-026-985-61
11	478.2	63.8	1617	2	US-08-378-939-9
12	476	63.5	9209	1	US-08-149-099C-3
13	476	63.5	9209	1	US-08-476-275-2
14	476	63.5	9209	2	US-08-478-967A-3
15	476	63.5	18986	2	US-08-819-866-2
16	476	63.5	18986	2	US-09-023-715-2
17	467.4	62.3	3282	1	US-08-276-852-154
18	467.4	62.3	3282	1	US-08-276-852-154
19	467.4	62.3	3282	1	US-08-899-575-154
20	467.4	62.3	3282	1	US-08-899-575-154
21	467.4	62.3	3282	1	US-08-899-575-154
22	467.4	62.3	3282	1	US-08-899-575-154
23	467.4	62.3	3282	5	PCT-US95-08743-154
24	467.4	62.3	13254	1	Sequence 169, App
25	467.4	62.3	13254	1	Sequence 169, App
26	467.4	62.3	13254	1	Sequence 169, App
27	467.4	62.3	13254	1	Sequence 169, App

28	467.4	62.3	13254	1	US-08-899-575-170	Sequence 170, App
29	467.4	62.3	13254	1	US-08-899-575-170	Sequence 170, App
30	467.4	62.3	13254	1	US-08-899-575-170	Sequence 170, App
31	467.4	62.3	13254	5	PCT-US95-08743-156	Sequence 170, App
32	467.4	62.3	13254	5	PCT-US95-08743-170	Sequence 170, App
33	462.4	61.7	2143	4	US-09-097-309-5	Sequence 9, Appl
34	462.4	61.7	2143	4	US-09-097-171A-9	Sequence 9, Appl
35	462.4	61.7	6550	4	US-09-422-712B-1	Sequence 1, Appl
36	461.2	61.5	1655	3	US-09-049-612A-21	Sequence 21, Appl
37	459.6	61.3	762	1	US-08-398-613A-57	Sequence 57, Appl
38	459.6	61.3	762	1	US-08-398-612A-57	Sequence 57, Appl
39	459.6	61.3	762	1	US-08-398-611A-57	Sequence 57, Appl
40	459.6	61.3	762	1	US-08-396-851A-57	Sequence 57, Appl
41	459.6	61.3	762	2	US-08-491-334A-57	Sequence 57, Appl
42	459.6	61.3	762	3	US-09-027-449-43	Sequence 43, Appl
43	459.6	61.3	762	3	US-08-804-444A-43	Sequence 43, Appl
44	459.6	61.3	762	3	US-09-026-985-43	Sequence 43, Appl
45	453.8	60.5	2178	1	US-08-463-587A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-027-449-68
Sequence 68, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Minipatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 8120 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-027-449-68
Query Match 66.0%; Score 495.2; DB 3; Length 8120;

REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-026-985-69

Query Match 65.1%; Score 488; DB 3; Length 800;
Best Local Similarity 79.4%; Pred. No. 6,7e-118;
Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 21 TCTCTCTCTCTGCTCACTAAGTGGGCGCTCCCAAGTCCCACTGCTGCAATCCGG 80
DB 63 TATGTTGTTTTTCTATTGCTACAAAGCGCTGAGCTGAGTTCAGTACGCTGCG 122
QY 81 CGCGAGGTCAGAGGCGGCGCTGCAAGTGTCTGTAAGCTAGGCGCTATAT 140
DB 123 CGGTGCGCTGCTGAGCGAGGCGCTGCTGTTGCTGCTGCAAGCTTCTGCTACTC 182
QY 141 TTTTCTAATTAATGATTCATGGTGCCTGAGCGCCCGGCGAGGCGCTGGAATGAT 200
DB 183 CTCTCGAGTACATATATGACATGGTCCGTCAGGCGCGGTAAGGCGCTGGAATGGGT 242
QY 201 GGGTGAATCTTACCGGCGCTGCTGAGCAGCGAATATACCGAATTTTAAAGCCGTG 260
DB 243 TGGATATATGATCTTCAATGCTGAAGTACGATATATCAAAAGTTCAAGGCGCTTT 302
QY 261 TACATATACCGGTACACTGCTGATAGTACATGATATACATGAGCTCTCCAGCTCGCAT 320
DB 303 CACTTATCTCGGACACACTTCAAAACAGACATACCTGAGATGAGAGCGCTCGTGC 362
QY 321 GAGGACACGCGCGCTATTATTCGCGCTTATTTTGGTTCAGCCGAATTTGTA 380
DB 363 TGAGGACACTGCGCTATATATCTGCAAGAGGGGATATATGCTTCAATGATGACTGGTT 422
QY 381 TTTTATGTTTGGGTCAGAGAACCTGCTGCTGCTGAGCGCGCTCCAGCAAGGGCC 440
DB 423 CTTCGACGCTGCGGCTCAAGGACCTGCTGCTGCTGCGCGCTCCAGCAAGGGCC 482
QY 441 ATGCGTCTTCCCTGGCGCGCTCTCTCCAGAGACCTTGGGGGCAAGGGCGCTGG 500
DB 483 ATGCGTCTTCCCTGGCGCGCTCTCTCCAGAGACCTTGGGGGCAAGGGCGCTGG 542
QY 501 CTGCGTCTGTCAGAGTACTTCCCGAAGCGGTGCTGCTGAGACTCTACTCCCTAG 560
DB 543 CTGCGTCTGTCAGAGTACTTCCCGAAGCGGTGCTGCTGAGACTCTACTCCCTAG 602
QY 561 GACCAGCGGCTGACACCTTCCCGGCTGCTCTACAGTCTCTACAGACTCTACTCCCTAG 620
DB 603 GACCAGCGGCTGACACCTTCCCGGCTGCTCTACAGTCTCTACTCTACTCCCTAG 662
QY 621 CAGGTGCTACAGTCTGCGCTCCAGACCTTGGGACCCAGACCTTACATCTGCAAGTGA 680
DB 663 CAGGTGCTACAGTCTGCGCTCCAGACCTTGGGACCCAGACCTTACATCTGCAAGTGA 722
QY 681 TCACAAAGCCAGCAACAGCAAGGTGAGCAAGAAATTTGAGCCCAATTTGTGACAAAC 740
DB 723 TCACAAAGCCAGCAACAGCAAGGTGAGCAAGAAATTTGAGCCCAATTTGTGACAAAC 782
QY 741 TCACACAT 748
DB 783 TCACACAT 790

RESULT 5
US-09-027-449-59
; Sequence 59, Application US/09027449

Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-027-449-59

Query Match 65.1%; Score 488; DB 3; Length 927;
Best Local Similarity 79.4%; Pred. No. 7e-118;
Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 21 TCTCTCTCTCTGCTCACTAAGTGGGCGCTCCCAAGTCCCACTGCTGCAATCCGG 80
DB 63 TATGTTGTTTTTCTATTGCTACAAAGCGCTGAGTTCAGTACGCTGCTGG 122
QY 81 CCGCGAGTCAAGAGCCAGGCGCTCAGTCAAGTGTCTGTAAGCTAGCGCTATAT 140
DB 123 CGGTGCGCTGCTGACAGCGGCGCTCACTCGTTGTCTCTGCAAGCTTCTGCTACTC 182
QY 141 TTTTCTAATTAATGATTCATGGTGCCTGAGCGCCCGGCGAGGCGCTGGAATGAT 200
DB 183 CTCTCGAGTACATATATACACTGCGGTCCGTCAGCGCGGTAAAGGCGCTGGAATGGGT 242
QY 201 GGGTGAATCTTACCGGCGCTGCTGAGCAGCGAATATACGAAATTTTAAAGCGGTG 260
DB 243 TGGATATATGATCTTCAATGCTGAACCTGATATATCAAAAGTTCAAGGCGCTTT 302
QY 261 TACTATGACGCTGACACTTCACTAGTACAGTATACATGAGCTCTCCAGCTGGCATC 320
DB 303 CACTTATCTCGGACAACTCCAAACACAGCATACCTGCAATACAGACCTGCTGCTG 362
QY 321 GAGGACACGCGCTGCTATATTTGCGCGCTATTTTTTTTGGTCTTACGCCCAATTTGTA 380
DB 363 TGAGGACACTGCGCTATATGCTGCAAGAGGGGATATATCGCTCAATGATGCTACTGGTT 422

QY 381 TTTGATGTTGGGTCAAGAACCTGTCTGTGAGCGCTCCACCAAGGCCCC 440
Db 423 CTTCGAGCTGTGGGTCAAGAACCTGTCTGTGAGCGCTCCACCAAGGCCCC 482
QY 441 ATCGGCTTCCCGGGGGGCGCTCTCCAAAGACCTGTGGGGGACAGCGGCCCTGGG 500
Db 483 ATCGGCTTCCCGGGGGGCGCTCTCCAAAGACCTGTGGGGGACAGCGGCCCTGGG 542
QY 501 CTGCGTGTCAAGGACTTCTCCCGAACCGGTGACGGTGTCTGGAACCTGAGCGCCCT 560
Db 543 CTGCGTGTCAAGGACTTCTCCCGAACCGGTGACGGTGTCTGGAACCTGAGCGCCCT 602
QY 561 GACGAGCGGCTGACACCTTCCCGGTCTCTACAGTCTGAGACTTCTCTCCCTAG 620
Db 603 GACGAGCGGCTGACACCTTCCCGGTCTCTACAGTCTGAGACTTCTCTCCCTAG 662
QY 621 CAGGCTGTGACCGGCTCTCAGAGCTTGGGACCCAGACTTCAATCTGAAAGCTGAA 680
Db 663 CAGGCTGTGACCGGCTCTCAGAGCTTGGGACCCAGACTTCAATCTGAAAGCTGAA 722
QY 681 TCACAGCCCGACCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGACAAAC 740
Db 723 TCACAGCCCGACCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGACAAAC 782
QY 741 TCACACAT 748
Db 783 TCACACAT 790

RESULT 6
US-08-804-444A-59
Sequence 59, Application US/0880444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Presta, Steven R.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-804-444A-59

Query Match 65.1%; Score 488; DB 3; Length 927;

Best Local Similarity 79.4%; Pred. No. 7e-118;
Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 21 TCTCTTCCTCCCTGTCACTAATGTCGGGCTCCACTCCCAAGTCAATGTGCAATCCGG 80
Db 63 TAGTGTGTTTTTCTATGTGTACAAAGCGGTAGCTGAGCTTACAGTAGTGCATCGG 122
QY 81 CGCGAGGTCAAGAACCGGAGGCGCTCAATCAAGTCTCTGTAAAGCTAGCGCTATAT 140
Db 123 CGGTGCGCTGTGAGCAGGAGGCGCTCACTCCGTTTCTGTGTGAGCTTCTGTACTC 182
QY 141 TTTTCTAATATATGATTAATGATGTCAGGTCGAGCGCCCGGAGCGGCTGGAATGAT 200
Db 183 CTCTTCAGTACTATATATGACAGTGGTCTGACGCGCCCGGTAAGGCTGAGTGGGT 242
QY 201 GGGTGAATCTTACCGGGCTCTGTAGACACCGAATATACCGAAATTTTAAAGACCGTGT 260
Db 243 TGGATATATGATCTCTTCATAGTGAAGTGAAGTATATATCAAAAGTCAAGGCGCTTT 302
QY 261 TACTATGACGCGTGAACCTTGCAGTACATGATATATATGAGCTCTCCAGCTGCATC 320
Db 303 CACTTATCTGCGCAACATCCAAAGAACACAGATACCTGCAGATGAAACAGCTGCGTGC 362
QY 321 GAGGACACGCGCTCTATATATGCGGCGCTTATTTTGTGTCTACCGGAATGTA 380
Db 363 TGAGGACACTGCGCTATATATGTCAGAGAGGGAATATGCTAACATGATGACTGTT 422
QY 381 TTTGATGTTGGGTCAAGAACCTGTCTGTGAGCGCTCCACCAAGGCCCC 440
Db 423 CTTCGAGCTGTGGGTCAAGAACCTGTCTGTGAGCGCTCCACCAAGGCCCC 482
QY 441 ATCGGCTTCCCGGGGGGCGCTCTCCAAAGACCTGTGGGGGACAGCGGCCCTGGG 500
Db 483 ATCGGCTTCCCGGGGGGCGCTCTCCAAAGACCTGTGGGGGACAGCGGCCCTGGG 542
QY 501 CTGCGTGTCAAGGACTTCTCCCGAACCGGTGACGGTGTCTGGAACCTGAGCGCCCT 560
Db 543 CTGCGTGTCAAGGACTTCTCCCGAACCGGTGACGGTGTCTGGAACCTGAGCGCCCT 602
QY 561 GACGAGCGGCTGACACCTTCCCGGTCTCTACAGTCTGAGACTTCTCTCCCTAG 620
Db 603 GACGAGCGGCTGACACCTTCCCGGTCTCTACAGTCTGAGACTTCTCTCCCTAG 662
QY 621 CAGGCTGTGACCGGCTCTCAGAGCTTGGGACCCAGACTTCAATCTGAAAGCTGAA 680
Db 663 CAGGCTGTGACCGGCTCTCAGAGCTTGGGACCCAGACTTCAATCTGAAAGCTGAA 722
QY 681 TCACAGCCCGACCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGACAAAC 740
Db 723 TCACAGCCCGACCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGACAAAC 782
QY 741 TCACACAT 748
Db 783 TCACACAT 790

RESULT 7
US-09-026-985-59
Sequence 59, Application US/09026985
Patent No. 613426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N.
APPLICANT: Presta, Steven R.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA


```

Db 1401 CTTTCAGAGTCAATATATGCACTGGGTCCGTGACGGCCCGGGTAAGGGCTGGAAATGGGT 1460
QY 201 GGGGAGATCTTACCGGGCTCTGGTAGACACCAATATACCGAAATTTTAAAGACCGGTGT 260
Db 1461 TGGATATATGATCTTCCCAATGGTGAAGACTCGTATATATCAAAAGTTCAGGGCGCTTT 1520
QY 261 TACATATGACGGGTGACCTTGTGACTAGTATACAGTATACAGGAGCTCTCCAGCTGGGATC 320
Db 1521 CACTTATCTCGCGACACCTCAAAAACACACATACCTGCAAGATGACACGAGCTGGGTGC 1580
QY 321 GGAGGACACGGCGCTGTATATATGCGCGCTTATTTTGGTGTAGCCCAATGGTGA 380
Db 1581 TGAGGACACCTCGCTCTATTTGTCAGAGAGGGGATTTATGCTTACAAATGGTACTGGTT 1640
QY 381 TTTTGTATTTGGGGTCAAGGAACCTTGCTGCTGAGCGCCCTCCACCAAGGGGCC 440
Db 1641 CTTGACACTGTGGGGTCAAGGAACCTTGCTGCTGAGCGCTCCACCAAGGGGCC 1700
QY 441 ATGGGCTTCCCGTGGGGCGCTCTCCAGAGACCTCTGGGGGACAGCGGCCCTGGG 500
Db 1701 ATCGGCTTCCCGTGGGACCTCTCCAGAGACCTCTGGGGGACAGCGGCCCTGGG 1760
QY 501 CTGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGGTGTGGTGAACCTGAGCGCCT 560
Db 1761 CTGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGGTGTGGTGAACCTGAGCGCCT 1820
QY 561 GACCAAGCGGCTGACACACTTCCCGGTGTCTTACAGTCTTACAGACTCTACTCCCTAG 620
Db 1821 GACCAAGCGGCTGACACACTTCCCGGTGTCTTACAGTCTTACAGACTCTACTCCCTAG 1880
QY 621 CAGGCTGTGACCGTGGCTCTCAGAGACTTGGGACCCAGACCTTACATGTGCAAGCTGAA 680
Db 1881 CAGGCTGTGACCGTGGCTCTCAGAGACTTGGGACCCAGACCTTACATGTGCAAGCTGAA 1940
QY 681 TCACAAGCCGACGACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAAC 740
Db 1941 TCACAAGCCGACGACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAAC 2000
QY 741 TCACACAT 748
Db 2001 TCACACAT 2008

```

```

TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6563 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-804-444A-61

Query Match 65.1%; Score 488; DB 3; Length 6563;
Best Local Similarity 79.4%; Pred. No. 1.2e-117;
Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

Db 21 TCTCTTCTCTCTCTCAAGTACTGTCGGGCTGCTCCACTCCCAAGTCAATGTCGTAATCCG 80
Db 1281 TATGTTGTTTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1340
QY 81 CGCCGAGTCAAGAAAGCCAGGGGCTCTGTAAGGTCTCTGTAAGCTTACGCGTATAT 140
Db 1341 CGGTGGCTGTGACAGCCAGGGGCTCTGTAAGGTCTCTGTAAGCTTACGCGTATAT 1400
QY 141 TTTTCTTATTTATTTGATTTAATGGGTGCTGACAGGGGCTCTGTAAGGTCTTAT 200
Db 1401 CTTCTCAGTCACTATATATGACGTGGTCTGACAGGGGCTCTGTAAGGTCTTAT 1460
QY 201 GGGTGAATTTTACCGGGGCTCTGTAAGGTCTGTAAGGTCTTAT 260
Db 1461 TGGATATATGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1520
QY 261 TACTATGACCGTGTGACACTTCTGACTAGTATGATGAGTCTTCAAGCTTCAAGCTGATC 320
Db 1521 CACTTTATCTCGGACACACCTCAAAACAGAGTACTGCAAGTGAAGAGCTGCGTGC 1580
QY 321 GAGGACACGGCGTCTTATTTATGCGCGCTTATTTTGGTGTGAGCCGAAATGTGA 380
Db 1581 TGAGGACACTGCGGTATATGCTGCAAGAGGGGATTTATGCTTACATGGTGTGCTGTT 1640
QY 381 TTTTGTATGTTGGGTGTAAGAAACCTTGCTGCTCTGACAGCCCTTCCACCAAGGGCCC 440
Db 1641 CTTGACAGTCTGGGGTCAAGGAACCTTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 1700
QY 441 ATCGGCTTCCCGTGGGCGCTCTCTCAAGAGACCTTGGGGGACAGGGGCTGGG 500
Db 1701 ATCGGCTTCCCGTGGGCGCTCTCTCAAGAGACCTTGGGGGACAGGGGCTGGG 1760
QY 501 CTGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGGTGTGTAAGCTTACAGCGCCT 560
Db 1761 CTGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGGTGTGTAAGCTTACAGCGCCT 1820
QY 561 GACCAAGCGGCTGACACACTTCCCGGTGTCTTACAGTCTTACAGACTTACTCTCTAG 620
Db 1821 GACCAAGCGGCTGACACACTTCCCGGTGTCTTACAGTCTTACAGACTTACTCTCTAG 1880
QY 621 CAGGCTGTGACCGTGGCTCTCAGAGACTTGGGACCCAGACCTTACATGTGCAAGCTGAA 680
Db 1881 CAGGCTGTGACCGTGGCTCTCAGAGACTTGGGACCCAGACCTTACATGTGCAAGCTGAA 1940
QY 681 TCACAAGCCGACGACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAAC 740
Db 1941 TCACAAGCCGACGACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGTGACAAAC 2000
QY 741 TCACACAT 748
Db 2001 TCACACAT 2008

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RESULT 10
US-09-026-985-61
; Sequence 61, Application US/09026985
; Patent No. 6133426

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GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P10583-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 6563 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-026-985-61

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Query Match 65.1%; Score 488; DB 3; Length 6563;
Best Local Similarity 79.4%; Pred. No. 1.2e-117;
Matches 378; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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QY 21 TCTCTCTCTCTCTCACTAGTACGCGCGGCTCACTCCCAAGTCCACAGTGCATCCGG 80
DB 1281 TATGTCGCTTTTCTATTGCTTACAAAGCGGTACGCTGAGGTTAGCTAGTCTGG 1340
QY 81 CGCGAGGCTCAGACAGCCAGGCGCTCAGTCAAGTGTCTCTAAGCTACGCTATAT 140
DB 1341 CGGTGCTGCTGCTCAGCAGCGGCGCTCAGTCCGTTGTCTGCTCAGAGCTTCTGCTACTC 1400
QY 141 TTTTCTAATATATGATTAATAGGCTGCTCAGAGCCCGCGGAGGCGCTGGAATGAT 200
DB 1401 CTCTCGAGTCACTATATATGAGGCGCTCAGAGCCCGGCTAAGGCGCTGGAATGAGT 1460
QY 201 GGGTGAATCTCTCGCGGCTCTGTAGCAGCAATATACGAAATTTTAAGACCGGT 260
DB 1461 TGATATATTGATCTCTTCCATGCTAACTAGCTATATCAAAAGTTCAGAGGCGCTT 1520
QY 261 TACTATAGCGCTGACACTTCTGACTAGTATACATGAGTCTTCCAGCTTCGATC 320
DB 1521 CACTTATATCTCGGACACATCCAAAACACAGCATACCTGAGATGAACCCGCGTGC 1580
QY 321 GGAGGACAGCGCGCTCTATTATTTGCGCGCTTATTTTGGTTCTAGCCGAATGGTA 380
DB 1581 TGAGGACACTGCGCTATATAGTCAAGAGGAGATTATGCTACAAATGCTGACTGTT 1640
QY 381 TTTGATGTTTGGGTCAGAGACCCGCTGCTCAGCTCTCAGAGCCCTCCACCAAGGCCC 440
DB 1641 CTTCGAGCTCTGGGTCAGAGAACCCGCTGCTCAGCTCTCCTCGGCTCCACCAAGGCCC 1700
QY 441 ATCGCTCTCCCGCTGCGCGCTCTCTCAGAGACCTCTGGGGGACAGGCGCGCTGGG 500

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DB 1701 ATCGCTCTCCCGCTGCGACCCCTCTCCAAAGACACCTCTGGGGGACAGCGCGCTGGG 1760
QY 501 CTGCGTGGTCAAGGACTACTTCCCGAACCAGGAGGAGGCTGTGGAAGTCAAGGCGCT 560
DB 1761 CTGCGTGGTCAAGGACTACTTCCCGAACCAGGAGGAGGCTGTGGAAGTCAAGGCGCT 1820
QY 561 GACGAGCGGCTGACACACCTTCCGCGCTGCTCTAGAGTCTCAGAGACTACTCCCTCAG 620
DB 1821 GACGAGCGGCTGACACACCTTCCGCGCTGCTCTAGAGTCTCAGAGACTACTCCCTCAG 1880
QY 621 CAGCGTGTGACCGCTGCTCTCAGAGCTTGGGACCCAGAGACTTCTGCAAGCTGA 680
DB 1881 CAGCGTGTGACCGCTGCTCTCAGAGCTTGGGACCCAGAGACTTCTGCAAGCTGA 1940
QY 681 TCACAAGCCACCAACACCAAGGTGAGCAAGAAAGTGGCCCAATCTGTGACAAAAC 740
DB 1941 TCACAAGCCACCAACACCAAGGTGAGCAAGAAAGTGGCCCAATCTGTGACAAAAC 2000
QY 741 TCACACAT 748
DB 2001 TCACACAT 2008

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RESULT 11
US-08-378-939-9
Sequence 9, Application US/08378939
Patent No. 5876961

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GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESS: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 35..92
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 93..1465

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Sequence 3, Application US/08478967A
Patent No. 5843439
GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
APPLICANT: HANNA, Nabli
APPLICANT: LEONARD, John E.
APPLICANT: NEWMAN, Roland A.
APPLICANT: REEF, Mitchell E.
APPLICANT: RASTETTER, William H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,967A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-478-967A-3

Query Match 63.5%; Score 476; DB 2; Length 9209;
Best Local Similarity 78.2%; Pred. No. 1.8e-114;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 ATGAAGTGGAGCTGGGTATTTCTCTTCCTCCCTGTCAGTAACTCCCGCGTCCACTCCCAA 60
DB 2401 ATGGTTGGAGGCTCATCTTCTGCTGTCGCTGCTAGCTAGCGGTGCTCCAG 2460
QY 61 GTCCAACTGCTGTCATCCGCGCCGAGTCAAGAACGAGGCGCTCAGTCAAGTGTCC 120
DB 2461 GTACAACTGACAGCTGCGGCTGAGCTGAGTGAAGCCCTGCGGCTCAGTGAAGATGTCC 2520
QY 121 TGTAAAGCTAGCGGCTATATTTTCTTAATTATTTGATTCAATGGGTGCTCAGGCCCC 180
DB 2521 TGCAGAGCTTCTGCTACACATTTACAGTTCATTAATATGACAGTGGGTAAACAGACACT 2580
QY 181 GGGCAGGCGCTGGAATGATGGGTGAGATCTTACCGGCGCTCTGGTGAACACCGAATPACC 240
DB 2581 GGTCTGGGCTGTGGAATGATGAGCTATTTATCCCGGAATGATGATCTTCTCAAT 2640

QY 241 GAAATTTTAAAGACCGTGTATATGACGCGTACACTTGTGACTAGTACATATPACATG 300
DB 2641 CAGAAATTCAAAGGACAGGCGCATTTGACTACAGACAAATCTCCAGACAGCCTACATG 2700
QY 301 GAGCTTCCAGCCCTGCGCATGCGAGACACAGGCGCTCTTTATTTGCGCCGTTATTTTTT 360
DB 2701 CAGCTCAGCAGCTGACATGAGAGACTCTCGGTCTATTTACTGTGCAAGATCAGACTT- 2758
QY 361 GGTCTTACCCGAAATTTGATTTGATTTGGGGTCAAGAAACCTGTGACTGTCTG 420
DB 2759 -ACTACGGCGGTGACTGTACTTCAATCTCTGCGGCGAGGAGACAGGTACCGTCT 2817
QY 421 AGCGCTCCACCAAGGCGCCATCGTCTTCCCTGCGCCCTCTCTCCAGACAGCCTCT 480
DB 2818 GCACCTGACACCAAGGCGCCATCGTCTTCCCTGCGACCTCTCTCCAGACAGCCTCT 2877
QY 481 GGGGACACAGGCGCCCTGCGCTGCTGCTGCTCAAGACTCTTCCCGAAGCGGTACGGTG 540
DB 2878 GGGGACACAGGCGCCCTGCGCTGCTGCTGCTCAAGACTCTTCCCGAAGCGGTACGGTG 2937
QY 541 TCGTGAACCTCAGCGCGCTGACAGCGCGCTGACACACTTCCGCGTGTCTACAGTCC 600
DB 2938 TCGTGAACCTCAGCGCGCTGACAGCGCGCTGACACACTTCCGCGTGTCTACAGTCC 2997
QY 601 TCAGGACTTACTCCTCTCAGAGCGGTGTCACCGTCCCTCAGACAGCTTGGGACCCAG 660
DB 2998 TCAGGACTTACTCCTCTCAGAGCGGTGTCACCGTCCCTCAGACAGCTTGGGACCCAG 3057
QY 661 ACCTACATCTGCAACGTAATTCACAGCCCGACAGACCAAGGTGACAAAGATGAG 720
DB 3058 ACCTACATCTGCAACGTAATTCACAGCCCGACAGACCAAGGTGACAAAGATGAG 3117
QY 721 CCCAATCTTGTGACAAACCTCACACAT 748
DB 3118 CCCAATCTTGTGACAAACCTCACACAT 3145

RESULT 15
US-08-819-866-2
Sequence 2, Application US/08819866
Patent No. 5830698
GENERAL INFORMATION:
APPLICANT: REEF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Reita
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,866
FILING DATE: 14-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-352
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448
A:Accession: S36265
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1118 <GRI>
A:Cross-references: EMBL:218846; NID:933121; PIDN:CAAV9298.1; PID:9393900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 476.00 Length: 122
Ratio: 4.250 Gaps: 1
Percent Similarity: 91.803 Percent Identity: 76.230

alignment_block:
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Align seg 1/1 to: S36265 from: 1 to: 118

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1 CAAGTCCAACTGCTGTCATCCGCGCCGAGTCAAGACAGCGGCGCTC 50
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSer 17
51 AGTCAAGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTAATGGA 100
17 rValLysValSerGlyLysAlaSerGlyTyrThrPheThrGlyTyrM 34
101 TTCAAATGGGTCGTCAGAGCCCGGCGAGGCGCTGGAATGATGGTGA 150
34 ethIstrpValArgGlnAlaProGlyGlnGlyLeuGlnLurPmetGlyTyr 50
151 ANCTACCGGGCTCTGGTAGCAGCGAATATACCGAAATTTAAAGACG 200
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyTyr 67
201 TGTACTATGACGCGTGCACACTTCGACTAGTACATGATACATGACCTC 250
67 gValThrIleThrArgAspThrSerAlaSerThrAlaTyrMetGluLeu 84
251 CCAGCTCGCATCGAGAGACAGCGCGCTCTATATTATTCGCGGCTATTT 300
84 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgAspPhe 100
301 TTTGTTCTACCCCAATTTGATTTTGTGGGGGTCAGGAACCT 350
101 LeuSerGly.....TyrLeuAspTyrTyrPGLyGlnGlyThrDe 113
351 GGTCACTGCTCTGACG 366
113 uValThrValSerSer 118
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seq_name: p1r2:S46393

seq_documentation_block:

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C:Accession: S46393

R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

A:Reference number: S46390; MUID:94254092

A:Accession: S46393

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-129 <FIG>
A:Cross-references: EMBL:231680; NID:9509786; PIDN:CAAB83485.1; PID:91335146
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 471.50 Length: 129
Ratio: 4.210 Gaps: 2
Percent Similarity: 86.822 Percent Identity: 72.093

alignment_block:

US-08-487-283a-12_COPY_58_423 x S46393 ..

Align seg 1/1 to: S46393 from: 1 to: 129

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1 CAAGTCCAACTGCTGTCATCCGCGCCGAGTCAAGACAGCGGCGCTC 50
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSer 17
51 AGTCAAGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTAATGGA 100
17 rValLysValSerGlyLysAlaSerGlyTyrThrPheThrGlyTyrM 34
101 TTCAAATGGGTCGTCAGAGCCCGGCGAGGCGCTGGAATGATGGTGA 150
34 ethIstrpValArgGlnAlaProGlyGlnGlyLeuGlnLurPmetGlyTyr 50
151 ANCTACCGGGCTCTGGTAGCAGCGAATATACCGAAATTTAAAGACG 200
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyTyr 67
201 TGTACTATGACGCGTGCACACTTCGACTAGTACATGATGACGCTC 250
67 pValThrMetThrArgAspThrSerIleSerThrAlaTyrMetGluLeu 84
251 CCAGCTCGCATCGAGAGACAGCGCGCTCTATATTATTCGCGGCT 294
84 erArgLeuArgSerAspAspThrAlaValTyrTyrCysAlaArgAspSer 100
295 ...TATTTTGGTCT.....AGCCGAATTTGATTTTGA 329
101 AlatyTyrTyrAspSerSerGlyTyrTyrSerAlaAsnTyrMetAs 117
330 TGTTTGGGTCAGGAACCTGTCACCTGTCGTCGAC 366
117 pValTyrPGLyLysGlyThrThrValThrValSerSer 129
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seq_name: p1r2:C30562

seq_documentation_block:

Ig heavy chain V region (27.7.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996

C:Accession: C30562

R:Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison,

J. Immunol. 142, 888-893, 1989

A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen

A:Reference number: A30562; MUID:89110066

A:Accession: C30562

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <SIK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality: 467.50 Length: 122
Ratio: 4.289 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 70.492

alignment_block:
US-08-487-283a-12_copy_58_423 x C30562

Align seg 1/1 to: C30562 from: 1 to: 119

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1 CAAGTCAACTGTGTCATCCGCGCCGAGGTCAAGAACCCAGGGCCTC 50
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1 GlnValGlnLeuGlnInserGlyAlaGluLeuMetLysProGlyAla 17
51 AGTCAAAAGTGTCTGTAAAGCTAGCGCTAATATTTTCTAATTATTTGA 100
||||| 119
17 rValLysIleSerCysLysAlaThrGlyTrpThrPheSerSerTyrrTrpI 34
51 TTCAATGGGTGCTCAGAGCCCGCGGCGAGGCGCTGGAATGATGGGTGAG 150
||||| 119
34 legLutrrPValLysGlnArgProGlyHisGlyLeuGlnTrpIleGlyGln 50
151 ATCTTACCGGGCTGTGTAGACCGGAATATACGAAATTTTAAAGACCG 200
||||| 119
51 llePheProGlySerGlySerThrAsnGlyArgLysPheLysGlyLys 67
201 TGTACTATGACCGCTGACACTTCGACTAGTACAGTATACATGAGCTCT 250
||||| 119
67 salatThrPheThrAlaAspThrSerSerAsnThrAlaTyrrMetGlnLeu 84
251 CCAGCTCGGATCGAGACACGCGCTATATTATTCGCGCGCTAATTTT 300
||||| 119
84 erSerLeuThrSerGluAspSerAlaValTyrrGlyCysAlaArgHisTy 100
301 TTGGGTCTACGCCGAATGTGATTTTGTATTTGGGTCAAGAACCCCT 350
||||| 119
101 TyrGlySerSerSer.....PheAlaTyrrTrpGlyGlnGlyThrLe 114
351 GGTCACGTCTCTCGAGC 366
114 uValThrValSerAla 119

seq_name: p1r2:E30562

seq_documentation_block:
Ig heavy chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: E30562
R:Slkder, S.K.; Borden, P.; Gruenzo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.H.
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idlotype but not the antigen-bi
A:Reference number: A30562; MUID:89110066
A:Accession: E30562
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SIK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

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alignment_scores:
Quality: 464.50 Length: 122
Ratio: 4.261 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 69.672

alignment_block:
US-08-487-283a-12_copy_58_423 x E30562

Align seg 1/1 to: E30562 from: 1 to: 119

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1 CAAGTCAACTGTGTCATCCGCGCCGAGGTCAAGAACCCAGGGCCTC 50
||||| 119
1 GlnValGlnLeuGlnInserGlyAlaGluLeuMetLysProGlyAla 17
51 AGTCAAAAGTGTCTGTAAAGCTAGCGCTAATATTTTCTAATTATTTGA 100
||||| 119
51 ATCTTACCGGGCTGTGTAGACCGGAATATACGAAATTTTAAAGACCG 200
||||| 119
51 llePheProGlySerGlySerThrAsnGlyArgLysPheLysGlyLys 67

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||||| 119
17 rValLysIleSerCysLysAlaThrGlyTrpThrPheSerSerTyrrTrpI 34
101 TTCAATGGGTGCTCAGAGCCCGCGGCGAGGCGCTGGAATGATGGGTGAG 150
||||| 119
34 legLutrrPValLysGlnArgProGlyHisGlyLeuGlnTrpIleGlyGln 50
151 ATCTTACCGGGCTGTGTAGACCGGAATATACGAAATTTTAAAGACCG 200
||||| 119
51 llePheProGlySerGlySerThrAsnGlyArgLysPheLysGlyLys 67
201 TGTACTATGACCGCTGACACTTCGACTAGTACAGTATACATGAGCTCT 250
||||| 119
67 salatThrPheThrAlaAspThrSerSerAsnThrAlaTyrrMetGlnLeu 84
251 CCAGCTCGGATCGAGACACGCGCTATATTATTCGCGCGCTAATTTT 300
||||| 119
84 erSerLeuThrSerGluAspSerAlaValTyrrGlyCysAlaArgHisTy 100
301 TTGGGTCTACGCCGAATGTGATTTTGTATTTGGGTCAAGAACCCCT 350
||||| 119
101 TyrGlySerSerSer.....PheAlaTyrrTrpGlyGlnGlyThrLe 114
351 GGTCACGTCTCTCGAGC 366
114 uValThrValSerAla 119

seq_name: p1r2:D30562

```

```

seq_documentation_block:
Ig heavy chain V region (27.4b.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: D30562
R:Slkder, S.K.; Borden, P.; Gruenzo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.H.
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idlotype but not the antigen
A:Reference number: A30562; MUID:89110066
A:Accession: D30562
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SIK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

alignment_scores:
Quality: 460.50 Length: 122
Ratio: 4.225 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 68.852

alignment_block:

US-08-487-283a-12_copy_58_423 x D30562

Align seg 1/1 to: D30562 from: 1 to: 119

```

1 CAAGTCAACTGTGTCATCCGCGCCGAGGTCAAGAACCCAGGGCCTC 50
||||| 119
1 GlnValGlnLeuGlnInserGlyAlaGluLeuMetLysProGlyAla 17
51 AGTCAAAAGTGTCTGTAAAGCTAGCGCTAATATTTTCTAATTATTTGA 100
||||| 119
17 rValLysIleSerCysLysAlaThrGlyTrpThrPheSerSerTyrrTrpI 34
101 TTCAATGGGTGCTCAGAGCCCGCGGCGAGGCGCTGGAATGATGGGTGAG 150
||||| 119
34 legLutrrPValLysGlnArgProGlyHisGlyLeuGlnTrpIleGlyGln 50
151 ATCTTACCGGGCTGTGTAGACCGGAATATACGAAATTTTAAAGACCG 200
||||| 119
51 llePheProGlySerGlySerThrAsnGlyArgLysPheLysGlyLys 67

```

```
201 TGTACTATGACGCGTACACTTGCAGTACAGTATACATGAGACCTCT 250
      :::::||||| ::::::::::::::::::::|
67 salAtherpherhralaasptHrSerSerasnHrAlaTyrmGlnLeuS 84
      |||||  ||||| ::::::::::::::::::::|
251 CCAGCCTCGATCGAGACGACGCGCTATATTATTCGCCGCTATTTT 300
      |||||  ||||| ::::::::::::::::::::|
84 erSerLeuThrSerGlnuSpSerAlaValTyTyCysAlaArgHsTy 100
      TTTGGTTCAGCCCAATTGTATTTTGTGGGTCAGGAGAACCTT 350
      ::::::::::| ||| ||||| ::::::::::|
101 TyrglySerSerSer.....PheAlaTyTTPGlyGlnGlyThre 114
      ||||| ::::::::::|
351 GGTCACTGTCTCGAC 366
      ||||| ::::::::::|
114 uValThrValSerAla 119
      ||||| ::::::::::|
seq_name: p1r2:D33548
seq_documentation_block:
Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Klips, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A:Reference number: A33548; MUID:89345575
A:Accession: D33548
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
```

```
alignment_scores:
Quality: 458.50      Length: 123
Ratio: 4.168        Caps: 1
Percent Similarity: 89.431      Percent Identity: 72.358
```

alignment_block:

US-08-487-283A-12_COPY_58_423 x D33548 ..

Align seg 1/1 to: D33548 from: 1 to: 123

```
1 CAAGTCCAACTGTGTCATCCGCGCGGAGGTCAAGAGCCAGGGCCCTC 50
||||| ::::::::::|
1 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaSe 17
51 AGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATATGGA 100
||||| ::::::::::|
17 rValLysValSerCysGlnuAlaSerGlyThrPheThrGlyHsTyrm 34
||||| ::::::::::|
101 TTCATGGGTGCGTACAGGCCCGCGGAGGCGCTGGAATGATGGGTGAG 150
:::::| ::::::::::|
34 ethHsTrpValArgGlnAlaProGlyGlnGlyLeuGlnuTrpMetGly 50
||||| ::::::::::|
151 ATCTTACCGGCGCTGTGTAGCACCGCAATATACGAAATTTTAAAGAC 200
||||| ::::::::::|
51 IleasnProasnSerGlyGlyThrAsnTyAlaGlnLysPheGlnGlyAr 67
||||| ::::::::::|
201 TGTACTATGACGCGTACACTTGCAGTACAGTATACATGAGACCTCT 250
||||| ::::::::::|
67 gValThrLeuThrArgAspThrSerIleasnThrAlaTyrmGlnLeuS 84
||||| ::::::::::|
251 CCAGCCTCGATCGAGACGACGCGCTATATTATTCGCCGCT...TAF 297
||| ::::::::::|
84 erArgLeuArgSerAspSprHrAlaValTyTyCysAlaArgAlaSer 100
||||| ::::::::::|
298 TTTTGTGCTTCAGCCCAATTGTATTTGTGGTGGGTCAAGGAAC 347
::: ||| ::::::::::|
101 TyrcysGlyTyTyrAspCysTyTyrThrPhePheAspTyTyrGlnGly 117
```

```
348 CCGTGTCACTGTCTCGAC 366
||||| ::::::::::|
117 rLeuValThrValSerSer 123
      ||||| ::::::::::|
seq_name: p1r2:S49530
```

seq_documentation_block:

anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999

C:Accession: S49530

R:Malnoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A:Description: Molecular characterization of natural human anti-Sm autoantibodies.

A:Reference number: S48797

A:Accession: S49530

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-135 <MAH>

C:Cross-references: EMBL:246348; NID:g560839; PIDN:CA86467.1; PID:g560840

C:Superfamily: immunoglobulin V region: immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

```
alignment_scores:
Quality: 457.00      Length: 122
Ratio: 4.311        Caps: 1
Percent Similarity: 86.885      Percent Identity: 73.770
```

alignment_block:

US-08-487-283A-12_COPY_58_423 x S49530 ..

Align seg 1/1 to: S49530 from: 1 to: 135

```
1 CAAGTCCAACTGTGTCATCCGCGCGGAGGTCAAGAGCCAGGGCCCTC 50
||||| ::::::::::|
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaSe 36
51 AGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATATGGA 100
||||| ::::::::::|
36 rValLysValSerCysLysAlaSerGlyTyThrPheThrGlyTyTyrm 53
||||| ::::::::::|
101 TTCATGGGTGCGTACAGGCCCGCGGAGGCGCTGGAATGATGGGTGAG 150
:::::| ::::::::::|
53 ethHsTrpValArgGlnAlaProGlyGlnGlyLeuGlnuTrpMetGly 69
||||| ::::::::::|
151 ATCTTACCGGCGCTGTGTAGCACCGCAATATACGAAATTTTAAAGAC 200
||||| ::::::::::|
70 IleasnProasnSerGlyGlyThrAsnTyAlaGlnLysPheGlnGlyAr 86
||||| ::::::::::|
201 TGTACTATGACGCGTACACTTGCAGTACAGTATACATGAGACCTCT 250
||||| ::::::::::|
86 gValThrMetThrArgAspSprHrSerIleSerThrAlaTyrmGlnLeuS 103
||||| ::::::::::|
251 CCAGCCTCGATCGAGACGACGCGCTATATTATTCGCCGCTATTTT 300
||||| ::::::::::|
103 erArgLeuArgSerAspSprHrAlaValTyTyCysAlaArgAlaArg 119
||||| ::::::::::|
301 TTTGGTTCAGCCCAATTGTATTTGTGGTGGGTCAAGGAACCTCT 350
||||| ::::::::::|
120 ThrGly.....TyraSnTyTTPGlyGlnGlyThre 130
||||| ::::::::::|
351 GGTCACTGTCTCGAC 366
||||| ::::::::::|
130 uValThrValSerSer 135
      ||||| ::::::::::|
seq_name: p1r2:PH0954
```

seq_documentation_block:

Ig heavy chain V region (G6+ CIL1-HEN) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0954
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880
 A:Accession: PH0954
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-132 <MAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:31-35/Region: immunoglobulin homology <IMM>
 F:36-50/Region: complementarity-determining 1
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: complementarity-determining 3
 F:99-120/Region: complementarity-determining 3

alignment_scores:
 Quality: 456.00 Length: 132
 Ratio: 4.183 Gaps: 2
 Percent Similarity: 82.576 Percent Identity: 69.697

alignment_block:
 US-08-487-283a-12_COPY_58_423 x PH0954 ..
 Align seg 1/1 to: PH0954 from: 1 to: 132

```

1 CAAGTCCAACTGGTGCATCCGCGCCGAGGTCAGAGCCAGGCGCTC 50
  |||||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlySerSe 17
51 AGTCAAAGTGTCTCTAAAGCTAGCGCTATATTTCTAATATATGA 100
  |||||||
17 rValLysValSerCysLysAlaSerGlyThrPheSerSerTyralai 34
101 TTCATGGGTGCGTCAGGCCCGCGGAGGCGCTGAAATGATGGTGAG 150
  |||||||
34 leSerTrpValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGly 50
151 ATCTTACCGGGCTCTGGTAGACACCGAATATACGAAATTTTAAAGCCG 200
  |||||||
51 IleIleProIlePheGlyThrAlaAsnTyralGlnLysPheGlnGlyAr 67
201 TGTACTATGAGCGGTGACACTGCTAGTACATATGATGAGGCTCT 250
  |||||||
67 gValThrIleThrAlaAspLysSerThrSerThrAlaTyMetGluLeu 84
251 CCAGCTCGGATCGAGACACGCGCTATATATGCGGCGT..... 294
  |||||||
84 erSerLeuArgSerGlnAspThrAlaValTyTrpCysAlaArgProHis 100
295 .....TATTTTGGTCTAGCCCGAATTTGTAATTTT.. 327
  |||||||
101 AlaSerIleAspAspPheTrpSerGlyTyTrpProAsnTyTrpTyTrp 117
328 .....GATGTTGGGTCAAGAACCCGTCACGTCTCGAGC 366
  |||||||
117 rGlnMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 132

```

seq_name: p1r2:PH0952
 seq_documentation_block:
 Ig heavy chain V region (G6+ CIL-SMI) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C:Accession: PH0952
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880

A:Accession: PH0952
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-128 <MAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:31-35/Region: immunoglobulin homology <IMM>
 F:36-50/Region: complementarity-determining 1
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: complementarity-determining 3
 F:99-116/Region: complementarity-determining 3

alignment_scores:
 Quality: 453.00 Length: 128
 Ratio: 4.156 Gaps: 2
 Percent Similarity: 85.156 Percent Identity: 71.875

alignment_block:
 US-08-487-283a-12_COPY_58_423 x PH0952 ..
 Align seg 1/1 to: PH0952 from: 1 to: 128

```

1 CAAGTCCAACTGGTGCATCCGCGCCGAGGTCAGAGCCAGGCGCTC 50
  |||||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlySerSe 17
51 AGTCAAAGTGTCTCTAAAGCTAGCGCTATATTTCTAATATATGA 100
  |||||||
17 rValLysValSerCysLysAlaSerGlyThrPheSerSerTyralai 34
101 TTCATGGGTGCGTCAGGCCCGCGGAGGCGCTGAAATGATGGTGAG 150
  |||||||
34 leSerTrpValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGly 50
151 ATCTTACCGGGCTCTGGTAGACACCGAATATACGAAATTTTAAAGCCG 200
  |||||||
51 IleIleProIlePheGlyThrAlaAsnTyralGlnLysPheGlnGlyAr 67
201 TGTACTATGAGCGGTGACACTGCTAGTACATATGATGAGGCTCT 250
  |||||||
67 gValThrIleThrAlaAspLysSerThrSerThrAlaTyMetGluLeu 84
251 CCAGCTCGGATCGAGACACGCGCTATATATGCGGCGT..... 294
  |||||||
84 erSerLeuArgSerGlnAspThrAlaValTyTrpCysAlaArgGlyGly 100
295 .....TATTTTGGTCT..AGCCGAATTTGTAATTTGATGT 332
  |||||||
101 AsnTyTrpAspTyTrpIleTrpLysSerTyTrpArgSerAsnAlaPheAsp 117
333 TTGGGGTCAAGAACCCGTCACGTCTCGAGC 366
  |||||||
117 eTrpGlyGlnGlyThrMetValThrValSerSer 128

```

seq_name: p1r2:S23623
 seq_documentation_block:
 Ig heavy chain V region precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S23623
 R:Olée, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defios, M.; Kozin, F.; Carson, D.A.
 J. Exp. Med. 175, 831-842, 1992
 A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
 A:Reference number: S23623; MUID:92156804
 A:Accession: S23623
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-171 <OLE>
 A:Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA4223.1; PID:g32011

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 453.00 Length: 126
Ratio: 4.194 Gaps: 2
Percent Similarity: 85.714 Percent Identity: 71.429

alignment_block:

US-08-487-283A-12_COPY_58_423 x S23623 ..

Align seg 1/1 to: S23623 from: 1 to: 171

```

1 CAAGTCCAACTGTCGATCCGCGCCGAGTCAGAACGCCAGGGCCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
51 AGTCAAAAGTGTCTGTAAGCTAGCGGCTATTTTCTTAATTATGGA 100
|||||
36 rValLysValSerCysGlySerGlyTyrThrPheThrAlaTyrGlnM 53
53 eHisTrpValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGlyTrp 69
101 TTCAATGGGTGCGTCAGGCCCGCGGAGCGGCTGGAATGATGGGTGAG 150
|||||
151 ATCTTACCGGGCTCTGTAGCAGCCAAATATACCGAAATTTTAAAGACCG 200
|||||
70 IleAsnProAsnSerGlyGlyThrGlyTyrGlyGlnLysPheGlnGlyAr 86
201 TGTACTATGACGCGTCGACACTGCTGACTAGTACGATATACGAGCTCT 250
|||||
86 gValThrLeuThrArgAspThrSerIleSerThrAlaTyrMetGlnLeuS 103
251 CCAGCTCGCATCGATGAGGACAGCGCGCTATATTATTCGCG...CGTTAT 297
|||||
103 eArgLeuThrSerAspThrAlaValTyrTyrCysAlaIleGlnIuYr 119
298 TTTTGTGTTCTGACG.....CCGAATTGATTTGATGTTGGGG 338
|||||
120 PheYrAspGlySerAspLeuLysProSerAspValPheAspIleTrpG1 136
339 TCAAGGAACCTGTCGATCTGTCGAGC 366
|||||
136 yGlnGlyThrMetValThrValSerSer 145

```

seq_name: p1r2:S31600

seq_documentation_block:

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence-revision 10-Nov-1995 #text-change 23-Jul-1999

C:Accession: S31600

R:Chislinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelier, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31600

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 <CUI>

A:Cross-references: EMBL:214165; NID:g30994; PIDN:CAA78534.1; PID:g30995

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality: 451.00 Length: 124
Ratio: 4.295 Gaps: 2
Percent Similarity: 84.677 Percent Identity: 72.581

alignment_block:

US-08-487-283A-12_COPY_58_423 x S31600 ..

Align seg 1/1 to: S31600 from: 1 to: 136

```

1 CAAGTCCAACTGTCGATCCGCGCCGAGTCAGAACGCCAGGGCCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
51 AGTCAAAAGTGTCTGTAAGCTAGCGGCTATTTTCTTAATTATGGA 100
|||||
36 rValLysValSerCysArgAlaSerGlyTyrThrPheThrSerTyrAspi 53
101 TTCAATGGGTGCGTCAGGCCCGCGGAGCGGCTGGAATGATGGGTGAG 150
|||||
53 leAsnTrpValArgGlnAlaThrGlyGlnGlyLeuGlnTrpMetGlyTrp 69
151 ATCTTACCGGGCTCTGTAGCAGCCAAATATACCGAAATTTTAAAGACCG 200
|||||
70 MetAsnProAsnSerGlyAsnThrGlyTyrAlaGlnLysPheGlnGlyAr 86
201 TGTACTATGACGCGTCGACACTTCTGACTAGTACGATATACATGAGCTCT 250
|||||
86 gValThrMetThrArgAsnThrSerIleSerThrAlaTyrMetGlnLeuS 103
251 CCAGCTCGCATCGATGAGGACAGCGCGCTATATTATTCGCGCGCTATTATT 300
|||||
103 eSerLeuAlaGlySerGlyAspThrAlaValTyrTyrCysAlaArg..... 117
301 TTTGTTCTTACGCCGAATTCG.....TATTTGATGTTTGGGGTCAGAC 344
|||||
118 .....TTPArgAspAlaPheAspIleTrpGlyGlnG1 128
345 AACCTGTCATCTGTCGAGC 366
|||||
128 yThrMetValThrValSerSer 135

```

seq_name: p1r2:S20783

seq_documentation_block:

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1995 #sequence-revision 20-Feb-1995 #text-change 21-Jan-2000

C:Accession: S20783

R:Mortari, F.; Wang, J.; Schroeder, H.W.

submitted to the EMBL Data Library, April 1992

A:Description: Analysis of human cord blood Ig heavy chain IGA and IGG repertoire.

A:Reference number: S20764

A:Accession: S20783

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: EMBL:211957; NID:g33899; PIDN:CAA78014.1; PID:g33890

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality: 450.50 Length: 124
Ratio: 4.171 Gaps: 2
Percent Similarity: 87.097 Percent Identity: 73.387

alignment_block:

US-08-487-283A-12_COPY_58_423 x S20783 ..

Align seg 1/1 to: S20783 from: 1 to: 121

```

1 CAAGTCCAACTGTCGATCCGCGCGGAGTCAAGAACGCCAGGGCCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 17
51 AGTCAAAAGTGTCTGTAAGCTAGCGGCTATTTTCTTAATTATGGA 100

```

[illegible]

```

seq_documentation_block:
I: heavy chain V region (G6+ T-L26) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0959
R:Marlin, T.; Dufify, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MID:92202880
A:Accession: PH0959
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-116 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-104/Region: complementarity-determining 3

```

```
alignment_scores:
  Quality: 450.00
  Ratio: 4.286
  Percent Similarity: 86.066
  Length: 1222
  Gaps: 2
  Percent Identity: 74.590
```

```
alignment_block:
```

Align seg 1/1 to: PH0959 from: 1 to: 116

```

1  CAAAGTCAACTGGTGCATCCGGGCGCCGAGTCAAGAACACAGGGGCTC 50
1  CAAAGTCAACTGGTGCATCCGGGCGCCGAGTCAAGAACACAGGGGCTC 50
1  GlnValIleuValGlnSerGlyValIleuValLysProGlySer 17
1  AGTCAAAAGTGTCTGTAAAGCTAGCGCGCTATATTTTTCATAATATGGA 100
51  AGTCAAAAGTGTCTGTAAAGCTAGCGCGCTATATTTTTCATAATATGGA 100
17  ValLysValSerCysLysAlaSerGlyGlyPheSerSerTyrAlaI 34
101  TTCAAATGGGTGCGTCAAGCCCCCGGGCAGAGGCGCTGCAATGATGGTGAG 150
111  TTCAAATGGGTGCGTCAAGCCCCCGGGCAGAGGCGCTGCAATGATGGTGAG 150

```

```

34  lesertrpValarglnalaprGinglynglyLuegluUrrpmetGlygyl 50
151 ATCTTACCGGGCTCTGTGACACCGCAATATTCGAAATTTTAAACACGG 200
51  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  lIlelleProllePheglylThralasmtYrAlaglnLpshelImolya 67
201 TGTACTATGACGGCGTGACACTTCGACTAGTACAGTATCATGGACCTCT 250
67  gValtThrllelhrAlaspluSerThrSerThrlaYrmetGluLeus 84
251 CCGAGCCGCGATCGGAGACACGGCCGCTATTATTCGCGGGGTATTTT 300
84  eIserLeuaYgSerGlnspHrAlaValYrTYrCysAlaArg..... 98
301 TTTGGTTCTAGACCCGAATTTGGTATTATTCATGCTTTGGGCGCAAGAACCT 350
99  ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99  .....GlyAspAsnTrp...PheAspTrpGlynglyThrle 111
351 GGTCACATGTCGAGC 366
111 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
111 uValtThrValSerSer 116

```

```

seq_name: plr2:PH0957
seq_documentation_block:
I9 heavy chain V region (G6+ CUL-BRA) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0957
J:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH09572; M0ID:92202860
A:Accession: PH0957
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-125 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-113/Region: complementarity-determining 3

```

```
alignment_scores:
  Quality: 449.50      Length: 130
  Ratio: 4.201        Gaps: 2
Percent Similarity: 82.308  Percent Identity: 70.000
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alignment_block:

Align seg 1/1 to: PH0957 from: 1 to: 12;

51 AGTCAAGTGTCTCTGTAAGACGTAGCGGGCTATATTTTCTAATTATTGA 1000
17 TAllySvAlsercYslySAlAlserGlyGlyThrPheSerSerTyAlAl 34
101 TTCATATGGGTGCGTCAGGCCCCCGGCGAGGGCTGGAAATGATGGGTGAG 1500
34 leaSnTrPvAlArGAlnAlAProGlyGlnGlyLeuGlnTrpMeGlyGly 50
151 AATCTTACCGGGCTGCTGTAACCGCAATATACCGAAATTTTAAAGACG 2000
51 TlelePcollePhelelylThrAlaSnTrYrAlaGlnLysPheGlnGlyAr 67

```

201 TGTACTATGACGCGTGAACCTTCGACTAGTACATATACATGAGACTCT 250
|||||:||||| ||| |||||:|||||:|||||:|||||
67 gValThrIleThrIleAspGluSerThrAsnThrAlaTyrMetGluLeu 84
251 CCAGCCTCGATCGAGAGACACGCGCTCTATTATTGCGGCGT..... 294
|||||:|||||:|||||:|||||:|||||:|||||
84 erSerIleuArgSerGluAspThrAlaValTyrTyrCysAlaArgAspGly 100
295 .....TATTTTGTGCTCTACGCCGCAATTGCTATT 326
|||||:|||||:|||||:|||||:|||||
101 CysSerGlyGlySerCysTyrPheTrpGly.....TrpPh 112
327 TGATGTTGGGGTCAAGAACCCCTGTCACCTGTCGAGC 366
|||||:|||||:|||||:|||||:|||||:|||||
112 eAspProTrpGlyGlnGlyThrIleuValThrValSerSer 125

```

OM of: US-08-487-283A-12_COPY_58_423 to: SwissProt_39:* out_format : pfs
Date: Jul 19, 2001 7:59 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

```
-MODEL-frame+ -n2p -model -DEV-x1p  
-O/cgcn2_1/USPTO_spool/US08487283/tnat_19072001.075205.246/app_query.fasta_1.444  
-DB-SwissProt_39 -OPTM-fastan -SUFFIX-tra.rsp -GAPOP=12.000  
-GABEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-DELOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX-biosum62  
-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE-pct  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pts  
-NORM-ext -MINLEN=0 -MAXLEN=200000000  
-USPR-US08487283_cgcn2_1.48 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPHY  
-WAIT -THREADS=1
```

Search information block:

Query: US-08-487-283A-12_COPY_58_423
Query length: 366
Database: SwissProt_39:*
Database sequences: 93435
Database length: 34255486
Search time (sec): 18.580000

score_list:

Sequence	Strid Orig	ZScore	EScore	Len	Documentation
SwissProt_39:HV07_MOUSE + 432.00	860.47	2.0e-40	139	P01751 mus musculus (mouse)	
SwissProt_39:HV1B_HUMAN + 429.00	855.99	4.2e-40	117	P01743 homo sapiens (human)	
SwissProt_39:HV01_MOUSE + 419.50	836.61	4.9e-38	121	P01745 mus musculus (mouse)	
SwissProt_39:HV1C_HUMAN + 414.00	823.81	2.1e-38	147	P01744 homo sapiens (human)	
SwissProt_39:HV1G_HUMAN + 403.00	802.76	3.4e-37	117	P23083 homo sapiens (human)	
SwissProt_39:HV11_MOUSE + 403.00	803.34	3.5e-37	137	P01755 mus musculus (mouse)	
SwissProt_39:HV12_MOUSE + 401.50	800.75	5.0e-37	117	P01756 mus musculus (mouse)	
SwissProt_39:HV50_MOUSE + 401.00	799.51	5.7e-37	120	P06529 mus musculus (mouse)	
SwissProt_39:HV03_MOUSE + 388.50	794.49	1.1e-36	120	P01747 mus musculus (mouse)	
SwissProt_39:HV13_MOUSE + 377.50	779.71	1.4e-36	117	P01757 mus musculus (mouse)	
SwissProt_39:HV4B_MOUSE + 377.50	779.17	6.8e-36	118	P03808 mus musculus (mouse)	
SwissProt_39:HV02_MOUSE + 383.50	762.97	5.3e-35	140	P01746 mus musculus (mouse)	
SwissProt_39:HV51_MOUSE + 377.00	751.45	2.8e-34	118	P06530 mus musculus (mouse)	
SwissProt_39:HV1A_HUMAN + 376.50	750.52	3.1e-34	117	P01742 homo sapiens (human)	
SwissProt_39:HV38_MOUSE + 370.00	737.31	1.7e-33	119	P01808 mus musculus (mouse)	
SwissProt_39:HV04_MOUSE + 365.00	727.42	6.1e-33	117	P01748 mus musculus (mouse)	
SwissProt_39:HV09_MOUSE + 365.00	727.42	6.1e-33	117	P01753 mus musculus (mouse)	
SwissProt_39:HV1H_HUMAN + 365.00	727.19	6.1e-33	120	P04021 homo sapiens (human)	
SwissProt_39:HV40_MOUSE + 364.00	725.26	7.9e-33	119	P01810 mus musculus (mouse)	
SwissProt_39:HV37_MOUSE + 363.00	723.25	1.0e-32	119	P01807 mus musculus (mouse)	
SwissProt_39:HV00_MOUSE + 359.00	715.60	2.8e-32	114	P01741 mus musculus (mouse)	
SwissProt_39:HV05_MOUSE + 357.00	711.35	4.8e-32	117	P01749 mus musculus (mouse)	
SwissProt_39:HV39_MOUSE + 353.50	704.24	1.2e-31	118	P01809 mus musculus (mouse)	
SwissProt_39:HV1E_HUMAN + 351.50	699.70	2.0e-31	125	P06526 homo sapiens (human)	
SwissProt_39:HV15_MOUSE + 351.50	698.94	2.0e-31	136	P01759 mus musculus (mouse)	
SwissProt_39:HV49_MOUSE + 350.00	697.28	2.9e-31	117	P06528 mus musculus (mouse)	
SwissProt_39:HV42_MOUSE + 350.00	697.28	2.9e-31	117	P06527 mus musculus (mouse)	
SwissProt_39:HV52_MOUSE + 349.50	696.28	3.3e-31	117	P01812 mus musculus (mouse)	
SwissProt_39:HV10_MOUSE + 349.00	695.27	3.8e-31	117	P01754 mus musculus (mouse)	
SwissProt_39:HV06_MOUSE + 347.00	691.25	6.3e-31	117	P01750 mus musculus (mouse)	
SwissProt_39:HV01_RAT + 346.50	688.51	7.4e-31	142	P01805 rat Rattus norvegicus (rat)	
SwissProt_39:HV41_MOUSE + 345.50	688.24	9.3e-31	117	P01811 mus musculus (mouse)	
SwissProt_39:HV3J_HUMAN + 344.50	685.93	1.2e-30	121	P01771 homo sapiens (human)	
SwissProt_39:HV18_MOUSE + 342.50	681.76	2.0e-30	123	P01787 mus musculus (mouse)	
SwissProt_39:HV19_MOUSE + 338.50	673.73	5.7e-30	123	P01788 mus musculus (mouse)	
SwissProt_39:HV21_MOUSE + 337.00	670.79	8.3e-30	122	P01789 mus musculus (mouse)	
SwissProt_39:HV21_MOUSE + 337.00	670.79	8.3e-30	122	P01790 mus musculus (mouse)	
SwissProt_39:HV22_MOUSE + 336.50	669.71	9.5e-30	123	P01791 mus musculus (mouse)	
SwissProt_39:HV16_MOUSE + 336.00	667.80	1.1e-29	136	P01783 mus musculus (mouse)	
SwissProt_39:HV23_MOUSE + 334.50	665.69	1.6e-29	123	P01792 mus musculus (mouse)	

SwissProt_39:HV1D_HUMAN + 331.00	658.59	3.9e-29	124	P01760 homo sapiens (huma
SwissProt_39:HV1E_HUMAN + 331.00	658.59	3.9e-29	124	P01761 homo sapiens (huma
SwissProt_39:HV14_MOUSE + 328.00	653.08	8.4e-29	117	P01758 mus musculus (mous
SwissProt_39:HV3D_HUMAN + 326.50	650.23	1.2e-28	115	P01765 homo sapiens (huma
SwissProt_39:HV3I_HUMAN + 324.50	645.90	2.1e-28	119	P01770 homo sapiens (huma

seq_name: SwissProt_39:HV07_MOUSE

seq_documentation_block:
ID HV07_MOUSE STANDARD; PRT; 139 AA.

AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

SEQUENCE FROM N.A.

RA STRAIN-C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.

RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).

CC -I- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLOWED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).

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CC EMBL: J00529; AAA38170.1; -.
CC PIR: A02034; MMS18.
CC InterPro: IPR003006; -.

DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL	1	19
FT CHAIN	20	139
FT DOMAIN	20	49
FT DOMAIN	50	54
FT DOMAIN	55	68
FT DOMAIN	69	85
FT DOMAIN	86	117
FT DOMAIN	118	124
FT DOMAIN	125	139
FT DISULFID	41	115
FT NON_TER	139	139
SO SEQUENCE	139 AA;	15419 MW; 1857DD4FD0C9F465 CRC64;

alignment_scores:
Quality: 432.00 Length: 123
Ratio: 4.037 Gaps: 2
Percent Similarity: 86.992 Percent Identity: 65.854

alignment_block:

US-08-487-283A-12_COPY_58_423 x HV07_MOUSE ..
Align seg 1/1 to: HV07_MOUSE from: 1 to: 139

1 CAAGTCAACTGTGTCATCCGGCGGAGGTCAAGAGAGAGGCGCTC 50
|||||
20 GlnvalGlnleuGlnInProGlyalactIueVallyssProclYalase 36

51 ACTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTTAATTATGA 100
 |||||
 36 rVallysleuSerCysAlaSerGlyThrPheThrSertYrTrpM 53
 |||||
 101 TTCANTGGGTGCTGAGCCCCCGGACAGGCGCTGGAATGAGGTGAG 150
 |||||
 53 eHISrPvalArgGlnAlaProGlyArgGlyLeuGluTrpIleGlyArg 69
 |||||
 151 ATCTTACCGGGCTGTGTAGCACCGCAATATACGAAATTTTAAAGACG 200
 |||||
 70 IleAspProAsnSerGlyGlyThrIlyTyraSngIuLysPheLysSerly 86
 |||||
 201 TGTACTATGACGCGTGCAGCTTCGACTAGTACAGTATCAGTACGAGCTCT 250
 |||||
 86 salAthrLeuThrValAspLysProSerSertThrAlaTyMetGluLeuS 103
 |||||
 251 CCAGCGTGTGATCGAGACGAGCGCGCTATATTATGCGCGCTAT... 297
 |||||
 103 erSerLeuThrSerGluAspSerAlaValTyTyrcysAlaArgTyraSp 119
 |||||
 298 TTTTWTGGTTCAGCCGCAATGTGATTTTGTATGTTGGGGTCAAGGAAAC 347
 |||||
 120 TyrTyrcGlySerSer.....TyrPheAspTyrtIrpGlyGlnGly 133
 |||||
 348 CCTGGTCACTGTCTGAGC 366
 |||||
 133 rThrLeuThrValSerSer 139
 |||||

seq_name: SwissProt_39:HV1B_HUMAN

seq_documentation_block:
 ID HV1B_HUMAN STANDARD; PRT; 117 AA.
 AC P01743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83144028; PubMed=6298778;
 RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
 RT "Evolutionary aspects of immunoglobulin heavy chain variable region
 (VH) gene subgroups";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: J00240; AA52988.1; -
 DR PIR: A02024; HAHUHG;
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12946 MW; 203F92FC60CD1FE7 CRC64;

alignment_scores:
 Quality: 429.00 Length: 98
 Ratio: 4.564 Gaps: 0
 Percent Similarity: 95.918 Percent Identity: 83.673

alignment_block:
 US-08-487-283A-12_COPY_58_423 x HV1B_HUMAN ..
 Align seg 1/1 to: HV1B_HUMAN from: 1 to: 117

1 CAAGTCCAACTGTGTGCAATCCGCGCCGAGCTCAAGAACCGAGGCGCTC 50
 |||||
 20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysLysProGlyAlaSe 36
 |||||
 51 AGCAAGGTGCTGTAAAGCTAGCGGCTATATTTTCTTAATTATGA 100
 |||||
 36 rVallysValSerCysLysAlaSerGlyTyrtThrPheAsnSertYrTrpM 53
 |||||
 101 TTCATGGGTGCTGTAGCACCGCAATATACGAAATTTTAAAGACG 200
 |||||
 53 eHISrPvalArgGlnAlaProGlyArgGlyLeuGluTrpIleGlyArg 69
 |||||
 151 ATCTTACCGGGCTGTGTAGCACCGCAATATACGAAATTTTAAAGACG 200
 |||||
 70 IleAsnProSerGlyGlySerThrSertYrAlaGlnLysPheGlnGlyAr 86
 |||||
 201 TGTACTATGACGCGTGCAGCTTCGACTAGTACAGTATCAGTACGAGCTCT 250
 |||||
 86 salAthrLeuThrValAspLysProSerSertThrAlaTyMetGluLeuS 103
 |||||
 251 CCAGCGTGTGATCGAGACGAGCGCGCTATATTATGCGCGCT 294
 |||||
 103 erSerLeuThrSerGluAspSerAlaValTyTyrcysAlaArgTyraSp 117
 |||||

seq_name: SwissProt_39:HV01_MOUSE

seq_documentation_block:
 ID HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MPC 11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81053741; PubMed=6253904;
 RA Zakut R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 RT region of immunoglobulin heavy chain MPC11";
 RL Nucleic Acids Res. 8:3591-3601(1980).
 CC -----
 CC REVISIONS.
 RA Zakut R., Cohen J., Givol D.;
 RL Nucleic Acids Res. 8:4839-4840(1980).
 CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
 CC FROM A MYELOMA THAT SECRETES IGG2B.
 DR PIR: A02027; GYMS11.
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56EDBF CRC64;

alignment_scores:
 Quality: 419.50 Length: 123
 Ratio: 3.921 Gaps: 2
 Percent Similarity: 86.992 Percent Identity: 60.976

alignment_block:
 US-08-487-283A-12_COPY_58_423 x HV01_MOUSE ..
 Align seg 1/1 to: HV01_MOUSE from: 1 to: 121

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07448; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19
FT NON_TER 20 117 IG HEAVY CHAIN V-I REGION V35.
FT 117 117
SQ SEQUENCE 117 AA; 13009 MW; BE1CE63F8CE97BD CRC64;

alignment_scores:
Quality: 403.00 Length: 98
Ratio: 4.380 Gaps: 0
Percent Similarity: 93.878 Percent Identity: 77.551

alignment_block:
US-08-487-283A-12_COPY_58_423 x HV1G_HUMAN ..

Align seg 1/1 to: HV1G_HUMAN from: 1. to: 117

1 CAAGTCCAACTGTCGATCCGCGCCGAGTCGAAGACCGAGGCGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyValGlnValLysProGlyAlaSe 36
51 AGTCAAACTGTCGATCCGCGCGGCGATATTTTCTAATTATGGA 100
|||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrGlyTyr 53
101 TTCATGGGTGGTCAGGCCCGCGGCGAGGCGCTGATGATGGGTAG 150
|||||
53 ethStrpValArgGlnAlaProGlyGlnGlyLeuGlnTyrPheMetGlyArg 69
151 ATCTTACCGGCGCTGTGTAGACACCGAATATACCGAAATTTTAAAGACCG 200
|||||
70 IleAspProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyArg 86
201 TGTACTATGACGCGCTGACACTTCGACTAGTACAGTATACATGAGCTCT 250
|||||
86 rValThrSerThrArgAspThrSerIleSerThrAlaTyrMetGlnLeu 103
251 CCAGCGCTCGATCGAGAGACGCGCGCTATATTGCGCGCGT 294
|||||
103 eArgGlnLeuArgSerAspThrValTyrTyrCysAlaArg 117

seq_name: SwissProt_39:HV11_MOUSE

seq_documentation_block:
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Botthell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00539; AAA38172.1; -
DR PIR; A02038; G2MS43.
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19
FT NON_TER 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

alignment_scores:
Quality: 403.00 Length: 122
Ratio: 3.990 Gaps: 1
Percent Similarity: 82.787 Percent Identity: 63.115

alignment_block:
US-08-487-283A-12_COPY_58_423 x HV11_MOUSE ..

Align seg 1/1 to: HV11_MOUSE from: 1 to: 137

1 CAAGTCCAACTGTCGATCCGCGCGGCGAGTCGAAGACCGAGGCGCTC 50
|||||
20 GlnValGlnLeuGlnGlnProGlyAlaGlnPheValLysProGlyAlaSe 36
51 AGTCAAACTGTCGATCCGCGCGGCGATATTTTCTAATTATGGA 100
|||||
36 rValLysLeuSerCysLysAlaSerGlyTyrThrPheThrSerTyrLeu 53
101 TTCATGGGTGGTCAGGCCCGCGGCGAGGCGCTGATGATGGGTAG 150
|||||
53 ethStrpValArgGlnAlaProGlyGlnGlyLeuGlnTyrPheMetGlyArg 69
151 ATCTTACCGGCGCTGTGTAGACACCGAATATACCGAAATTTTAAAGACCG 200
|||||
70 IleAspProAsnSerGlyGlyThrTyrAsnGlnLysPheArgSerIle 86
201 TGTACTATGACGCGCTGACACTTCGACTAGTACAGTATACATGAGCTCT 250
|||||
86 sAlaThrLeuThrIleAspLysProSerSerThrAlaTyrMetGlnLeu 103
251 CCAGCGCTCGATCGAGAGACGCGCGCTATATTGCGCGCGTATTTT 300
|||||
103 eArgLeuThrSerGlnAspSerAlaValTyrTyrCysAlaArgTyrArg 119
301 TTTGGTCTGACCGCAATGATTTTGGATGTTGGGTCGAAGACCGCT 350
|||||
120 LeuGlyArg.....TyrPheAspTyrTrpGlyGlnGlyThr 132
351 GGTCACTGTCTCGAC 366
132 rLeuThrValSerSer 137

seq_name: SwissProt_39:HV12_MOUSE

seq_documentation_block:
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;

21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MOPC 104E.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
[1]
SEQUENCE.
MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
"Complete amino acid sequence of a mouse mu chain: homology among
heavy chain constant region domains";
Biochemistry 21:5415-5424(1982).
-1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MHMS4E.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12963 MW; 3CF8ACE4BE47E41 CRC64;

alignment_scores:

Quality: 401.50 Length: 122
Ratio: 3.861 Gaps: 1
Percent Similarity: 85.246 Percent Identity: 59.836

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV12_MOUSE ..

Align seg 1/1 to: HV12_MOUSE from: 1 to: 117

```
1 CAAGTCCAACTGTCGCAATCCGGCCGAGTCAAGAACCGAGGCGCTC 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1 GlnValGlnLeuGlnGlnSerGlyProGlnLeuValLysProGlnAlaLase 17
51 AGTCAAAGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTATTTGA 100
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
17 rValLysMetSerCysLysAlaSerGlyTyrThrPheThrAspTyrTrpM 34
101 TTCAAATGGGCGCTCAGAGCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
34 eTyrStrValLysGlnSerHisGlyLysSerLeuGlnTyrPheLeuGlyAsp 50
151 ATCTTACCGGCGCTCGTACGACCGAATATCCGAAATTTTAAACCG 200
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
51 IleAsnProHisAsnGlnGlyThrSerTyrAsnGlnLysPheLysGlyLys 67
201 TGTACTATGACCGCGTACACTTGCAGTACAGTATACATGAGAGCTCT 250
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
67 salathrLeuthrValAspLysSerSerSerThrAlaTyrMetGlnLeuA 84
251 CCAGCTCGGATCGAGAGACAGCGCGCTATATTTGCGCGCTTATTTT 300
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
84 snSerLeuthrSerGlnAspSerAlaValTyrTyrCysAlaArgAspTyr 100
301 TTTGGTTCTAGCCCGAATGTTTGTATTTGATGTTGGGTCAGAGAACCT 350
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
101 .....AspTyrTyrPheAspValTrpGlyAlaGlyThrTh 112
351 GGTCACTGTCTCGAGC 366
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
112 rValThrValSerSer 117
```

seq_name: SwissProt_39:HV50_MOUSE

seq_documentation_block:
ID HV50_MOUSE STANDARD; PRT: 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Boyens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes";
EMBO J. 3:517-523(1984).
DR PIR: A02037; MHMS15.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453FA26F09834 CRC64;

alignment_scores:

Quality: 401.00 Length: 122
Ratio: 3.819 Gaps: 1
Percent Similarity: 86.066 Percent Identity: 60.656

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV50_MOUSE ..

Align seg 1/1 to: HV50_MOUSE from: 1 to: 120

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1 CAAGTCCAACTGTCGCAATCCGGCCGAGTCAAGAACCGAGGCGCTC 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1 GlnValGlnLeuGlnGlnSerGlyProGlnLeuValLysProGlnAlaLase 17
51 AGTCAAAGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTATTTGA 100
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
17 rValAsnLeuSerCysLysAlaSerGlyTyrThrPheThrSerTyrTrpM 34
101 TTCAAATGGGCGCTCAGAGCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
34 eHisTyrPheArgGlnArgProGlnGlnGlyLeuGlnTyrPheLeuGly 50
151 ATCTTACCGGCGCTCGTACGACCGAATATCCGAAATTTTAAACCG 200
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
51 IleAsnProSerAsnGlnGlyThrAsnTyrAsnGlnLysPheLysSerLys 67
201 TGTACTATGACCGCGTACACTTGCAGTACAGTATACATGAGAGCTCT 250
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
67 salathrLeuthrValAspLysSerSerSerThrAlaTyrMetGlnLeuA 84
251 CCAGCTCGGATCGAGAGACAGCGCGCTATATTTGCGCGCTTATTTT 300
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
84 eThrProThrSerGlnAspSerAlaValTyrTyrCysAlaArgTyrPasp 100
301 TTTGGTTCTAGCCCGAATGTTTGTATTTGATGTTGGGTCAGAGAACCT 350
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
101 Tyr.....GlnGlyAspArgTyrPheAspValTrpGlyThrGlyThrTh 115
351 GGTCACTGTCTCGAGC 366
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
115 rValThrValSerSer 120
```

seq_name: SwissProt_39:HV03_MOUSE

seq_documentation_block:
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Stekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC PIR; A02028; HWSG7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

alignment_scores:
Quality: 398.50 Length: 123
Ratio: 3.946 Gaps: 2
Percent Similarity: 82.114 Percent Identity: 62.602

alignment_block:

US-08-487-283A-12_COPY_58_423 x HV03_MOUSE ..

Align seg 1/1 to: HV03_MOUSE from: 1 to: 120

```
4 GTCCAACTGTCGAATCCGCGCCGAGTCAAGAAGCCAGGGCCCTCACT 53
||||| ||||||| ||||| ||||| ||||| ||||| ||||| |||||
1 ValGlnLeuGlnGlnSerGlyAlaGluLeuValArgAlaGlySerSerVa 17
54 CAAGTGTCTGCTAAAGCTAGCGGCTATATTTTCTAATTAATGATTC 103
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 llyMetSerCysIysAlaSerGlyTyrThrPheThrSerTyrGlyIleA 34
104 AATGGTCGTCAGGCCCGCCGCGGCGCTGATGATGGGTGGAGATC 153
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 snrPValIysGlnArgProGlyGlnGlyLeuGluTrpIleGlyTyrIle 50
154 TTACGGGCTCTGTAGACACCAATATACCAAAATTTTAAAGACGCT 203
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 AsnProGlyAsnGlyTyrThrIysTyrAsnGlyIuLysPheIysGlyIysTh 67
204 TACTATGACGGCTGACACTTCGACTAGTACATATACATGAGACTCTCA 253
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuArgS 84
254 GCTTCGCGATCGGAGACACGCGCTCTATATATGCGCGCT.....TAT 297
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 erLeuThrSerGlnAspSerAlaValTyrPheCysAlaIArgSerValTyr 100
298 TTTTGGTTCTAGCCCAATGATTTTGAAGTTTGGGTCACAGAAC 347
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 TyrIglyIysSer.....TyrTyrPheAspTyrTrpIglyIglyIth 114
348 CCGGTCACATGCTCTGAGC 366
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
114 rThrLeuThrValSerSer 120
```

seq_name: SwissProt_39:HV13_MOUSE
seq_documentation_block:
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P0157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments."
RL Nature 283:35-40(1980).
CC -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC PIR; A26242; MHMSJ5.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
FT SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

alignment_scores:
Quality: 397.50 Length: 122
Ratio: 3.859 Gaps: 1
Percent Similarity: 84.426 Percent Identity: 59.836

alignment_block:

US-08-487-283A-12_COPY_58_423 x HV13_MOUSE ..

Align seg 1/1 to: HV13_MOUSE from: 1 to: 117

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1 CAAGTCCCACTGTCGAATCCGCGCCGAGTCAAGAAGCCAGGGCCCTC 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GluValGlnLeuGlnGlnSerGlyProGluLeuValIysProGlyAlaSe 17
51 AGTCAAGTGTCTGCTAAAGCTAGCGGCTATATTTTCTAATTAATGGA 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 rValIysMetSerCysIysAlaSerGlyTyrThrPheThrAspTyrIym 34
101 TTCAAATGGTGCCTCAGGCCCGCCGCGGCGCTGAGATGGATGGTGAG 150
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 etLysrPValIysGlnSerHisGlyIysSerLeuGluTrpIleGlyAsp 50
151 ATCTTACCGGCTCTGTAGACACCAATATACCAAAATTTTAAAGACG 200
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 lIAsnProAsnAsnGlyIThrSerTyrAsnGlnIysPheIysGlyIy 67
201 TGTACTATACCGCGCTGACACTTCGACTAGTACATATATACATGAGGCT 250
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 sAlaThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuA 84
251 CCAAGCTCGCATCGGAGACACGCGCTCTATATATGCGCGCTATATTT 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 snSerLeuThrSerGlnAspSerAlaValTyrTyrCysAlaIArgAspArg 100
301 TTTGGTTCTAGCCCAATGATTTTGAAGTTTGGGTCACAGAACCT 350
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 Tyr.....TrpTyrPheAspValTrpIglyIglyIth 112
351 GGTACATGCTCTGAGC 366
```

|||||
112 rValthrValSerSer 117

seq_name: SwissProt_39:HV48_MOUSE

seq_documentation_block:

ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
RL PIR: A02033; HVMSG7.
DR InterPro; IPR003006; .
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 20
FT DOMAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SO SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

alignment_scores:
Quality: 392.50 Length: 124
Ratio: 3.886 Gaps: 2
Percent Similarity: 81.452 Percent Identity: 61.290

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV48_MOUSE

Align seg 1/1 to: HV48_MOUSE from: 1 to: 138

1 CAAGTCCAACTGCTGCAATCCGGCGCGAGTCAGACAGACGGGCGCTC 50
|||||
20 GlnValGlnLeuGlnGlnProGlyAlaGlnLeuValLysProGlyAlaSe 36
51 AGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATTTGA 100
|||||
36 rValGlnLeuSerCysAlaSerGlyHisThrPheThrAsnTyrTrpI 53
101 TTCATGGGTGCTGACAGCCCGCGGCGAGGCGCTGAATGATGGGTGAG 150
|||||
53 LeHisrTrpValLysGlnArgProGlyGlnLysLeuGlnLysTrpIleGlu 69
151 ATCTTACCGGGCTCTGGTAGCACCAGCAATATACGAAATTTTAAAGACG 200
|||||
70 IleAsnProAsnAspLysArgSerAsnTyrAsnGlnLysPheLysAsnLys 86
201 TGTACTATAGACCGCGACACTCGACTACTACATGATGAGAGCTCT 250
|||||
86 sAlaThrLeuThrValAspLysSerSerThrAlaTyrMetGlnLeuIns 103
251 CCAGCTGCGATCGAGAGACAGCGCGCTATATTATTCGCGCGTTATTTT 300

|||||
103 erSerLeuThrProGlnGlnPheAlaValTyrTyrGlyAlaArg..... 117
301 TTGGTTCAGCCCGCAATGTAT.....TTGATGTGTGGGCTCAGG 344
|||||
118SerAspGlyTyrTyrAsnTrpPheValTyrTrpGlnGln 131
345 AACCTGTCAGTCTCGAGC 366
|||||
131 yThrLeuValThrPheSerAla 138

seq_name: SwissProt_39:HV02_MOUSE

seq_documentation_block:

ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 9367 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT Immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00493; AAA38128.1; .
DR PIR; A02028; HVMSG7.
DR InterPro; IPR003006; .
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SO SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

alignment_scores:
Quality: 383.50 Length: 123
Ratio: 3.760 Gaps: 2
Percent Similarity: 82.927 Percent Identity: 60.163

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV02_MOUSE

Align seg 1/1 to: HV02_MOUSE from: 1 to: 140

1 CAAGTCCAACTGCTGCAATCCGGCGCGAGTCAGACAGACGGGCGCTC 50
|||||
20 GlnValGlnLeuGlnGlnProGlyAlaGlnLeuValLysProGlyAlaSe 36
51 AGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATTTGA 100
|||||
36 rAllyLysMetSerCysLysAlaSerGlyThrPheThrSerTyrGlyI 53
101 TTCATGGGTGCTGACAGCCCGCGGCGAGGCGCTGAATGATGGGTGAG 150
|||||


```

1 CAAGTCCAACTGGTGCATTCGGCCGAGGTCAAGAAGCCAGGGGCTC 50
  |||||||
1 GluValGlnLeuValGlnSerGlyAlaGlnValLysProGlySer 17
  |||||||
51 ACTCAAGTCTCCTGTAAAGCTAGCGGCTATATTTTCTAATTATTGGA 100
  |||||||
17 ValLysValSerCysLysAlaSerGlyGlyThrPheSerArgSerAlaI 34
  |||||||
101 TTCAAATGGGTGCGTCAGCGCCCGGCGACGGGCTGCAATGATGGGTAG 150
  |||||||
34 LeuLeuPValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGly 50
  |||||||
151 ACTTACCGGGGCTCTGTAGCACCGCAATATACCAAAATTTTAAAGCCG 200
  |||||||
51 IleValProMetPheGlyProProAsnTrpAlaGlnLysPheGlnGlyAr 67
  |||||||
201 TGTACTATGACCGCTGTGACACTTCGACTAGTACATGATGAGAGCTCT 250
  |||||||
67 GValThrIleThrAlaAspGlnSerThrAsnThrAlaTyrMetGluLeuS 84
  |||||||
251 CCAGCCTGCATCGGAGGACACGGCCGCTATATTTGCGCGCGTATATTT 300
  |||||||
84 eSerLeuArgSerGluAspThrAlaPheTyrPheCysAlaGlyGlyTyr 100
  |||||||
301 TTTCGTTCTAGCCCGAATGCTATTTGATGTTGGGTCAGAGACCTCT 350
  |||||||
101 GlyIleTyrSerProGlnGluTyr.....AsnGlyGlyLe 112
  |||||||
351 GGTCACTGCTCGAGC 366
  |||||||
112 uValThrValSerSer 117

```

seq_name: SwissProt_39:HV38_MOUSE

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seq_documentation_block:
ID HV38_MOUSE STANDARD: PRT: 119 AA.
AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE-79223895; PubMed-111245;
RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RT Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR: A02078; AVMS76.
DR HSSP: P01810; 2FBI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT NON TER 119 119
SQ SEQUENCE 119 AA: 13169 MW: BC38CC84E6EA00E8 CRC64;

```

alignment_scores:
 Quality: 374.00 Length: 123
 Ratio: 3.631 Gaps: 2
 Percent Similarity: 83.740 Percent Identity: 54.472

alignment_block:
 US-08-487-283a-12_COPY_58_423 x HV38_MOUSE ..

Align seg 1/1 to: HV38_MOUSE from: 1 to: 119

```

1 CAAGTCCAACTGGTGCATTCGGCCGAGGTCAAGAAGCCAGGGGCTC 50
  |||||||
1 GluValLysLeuLeuGlnSerGlyGlyGlyLeuValGlnProGlyLys 17
  |||||||
51 ACTCAAGTCTCCTGTAAAGCTAGCGGCTATATTTTCTAATTATTGGA 100
  |||||||
17 LeuLysLeuSerCysAlaAlaSerGlyPheAspPheSerArgTyrTrp 34
  |||||||
101 TTCAAATGGGTGCGTCAGCGCCCGGCGACGGGCTGCAATGATGGGTAG 150
  |||||||
34 eSerTrpValArgGlnAlaProGlyLysGlyLeuGluTrpIleGlyGly 50
  |||||||
151 ACTTACCGGGGCTCTGTAGCACCGCAATATATACCAAAATTTTAAAGCCG 200
  |||||||
51 IleAsnProAspSerSerThrIleAsnTyrThrProSerLeuLysAsp 67
  |||||||
201 TGTACTATGACCGCTGTGACACTTCGACTAGTACATGATGAGAGCTCT 250
  |||||||
67 sPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnMetS 84
  |||||||
251 CCAGCCTGCATCGGAGGACACGGCCGCTATATTTGCGCGGCTAT... 297
  |||||||
84 eLysValArgSerGluAspThrAlaLeuTyrTyrCysAlaArgLeuGly 100
  |||||||
298 TTTCGTTCTAGCCCGAATGCTATTTGATGTTGGGTCAGAGAAC 347
  |||||||
101 TyrTyrGly.....TyrPheAspValTrpGlyAlaGly 112
  |||||||
348 CCTGCTACTGCTCGAGC 366
  |||||||
112 rThrValThrValSerSer 118

```



```

301 TTGGTCTACCCGCAATGCTAT.....TTTGATTTGGGCTCAGG 344
    ::::: ||||| ||||| |||||
101 TTTValValValProAlaAlaPheSerArgPheAspTyrTrpGlyIngl 117
    ||||| ||||| ||||| ||||| |||||
345 AACCGTGTCTGCTGCTCGAGC 366
    ||||| ||||| ||||| ||||| |||||
117 yThrLeuValThrValSerSer 124

```

seq_name: sp_human:Q9UL94

seq_documentation_block:

```

ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AF035020; AAD56256.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 119
FT NON_TER 119
SO SEQUENCE 119 AA; 13205 MW; 13664F5345FA16E CRC64;

```

alignment_scores:

```

Quality: 451.50 Length: 122
Ratio: 4.142 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 71.311

```

alignment_block:

US-08-487-283a-12_COPY_58_423 x Q9UL94 ..

Align seg 1/1 to: Q9UL94 from: 1 to: 119

```

1 CAAGTCCAACTGTGCAATCCGGCCGCGAGGTCAAGACGAGGCGCTC 50
    ::::: ||||| ||||| ||||| |||||
1 GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAla 17
    ||||| ||||| ||||| ||||| |||||
51 AGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTATTTGA 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 TValLysValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrM 34
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 TTCATGGGTGCTCAGCCCGCGGCGAGGCGCTGCAATGATGATGAGT 150
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 eHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTyr 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 ATCTTACCGGCTGTGTAGCACCGCAATATACCGAAATTTTAAAGCCG 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 IleAsnProAsnSerTrpThrAsnTyrAlaGlnLysPheGlnGly 67
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 TGTACTATGACGCGGTGACACTTCGACTAGTACATGATGAGAGCTCT 250
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 sValThrMetThrLysAspThrSerLysSerThrAlaTyrMetGlnLeu 84
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 CCAGCGTGCATCGAGACAGCGCCGCTATATTTGCGGCGCTTATTTT 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

84 eArgLeuArgSerAspAspThrAlaValTyrTyrCysAlaArg..... 98
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 TTGGTCTACCCGCAATGCTATTTGATGTTGGGCTCAGGAACCT 350
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
99 ..GlyGlyGlyArgGlyLeuTrpPheAspProTrpGlyGlnGlyThrLe 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 GTTCACTGTCTCGAGC 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
114 uValThrValSerSer 119

```

seq_name: sp_human:Q9UL95

seq_documentation_block:

```

ID Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AF035019; AAD56255.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 125
FT NON_TER 125
SO SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

```

alignment_scores:

```

Quality: 446.50 Length: 125
Ratio: 4.096 Gaps: 1
Percent Similarity: 87.200 Percent Identity: 69.600

```

alignment_block:

US-08-487-283a-12_COPY_58_423 x Q9UL95 ..

Align seg 1/1 to: Q9UL95 from: 1 to: 125

```

1 CAAGTCCAACTGTGCAATCCGGCCGCGAGGTCAAGACGAGGCGCTC 50
    ::::: ||||| ||||| ||||| |||||
1 GluValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAla 17
    ||||| ||||| ||||| ||||| |||||
51 AGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTATTTGA 100
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 TValLysValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrM 34
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 TTCATGGGTGCTCAGCCCGCGGCGAGGCGCTGCAATGATGATGAGT 150
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 eHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTyr 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 ATCTTACCGGCTGTGTAGCACCGCAATATACCGAAATTTTAAAGCCG 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysValGlnGlyAr 67
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 TGTACTATGACGCGGTGACACTTCGACTAGTACATGATGAGAGCTCT 250
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 gValThrMetThrArgAspThrThrLysSerThrAlaTyrMetGlnLeu 84
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

251 CCAAGCCGATCGAGACACGCGCTATATATGGCCGCTATTTT 300
 11. |||||
 84 erArgLeuArgSerAspAspThrAlaValTyrTyrCysAlaArgSerGln 100
 301 TTTCGT.....TCTAGCCCAATGATTTTGATGTTGGGCTCA 341
 101 GYGLYGLYArgIleAlaAlaGlyAspAlaPheAspIleTyrGly 117
 342 AGGAACCCGTCACGTCGACG 366
 117 nglyThrMetValThrValSerSer 125

seq_name: sp_human:Q9UL89

seq_documentation_block:
 ID Q9UL89 PRELIMINARY; PRT: 116 AA.
 AC Q9UL89;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 16, Last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN
 EMBL: AF035025; AAD56261.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 116
 SO SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

alignment_scores:
 Quality: 445.00 Length: 118
 Ratio: 4.320 Gaps: 1
 Percent Similarity: 87.288 Percent Identity: 73.729

alignment_block:
 US-08-487-283A-12_COPY_58_423 x Q9UL89 ..

Align seg 1/1 to: Q9UL89 from: 1 to: 116

13 GTGCAATCCGCGCCGAGTCACAGACCGAGGCGCTCATGCAAGTCTC 62
 |||||
 1 ValGlnSerIylAlaGluValIylsLysProGlySerSerValIylsVal 17
 63 CTGTAAAGCTAGCGGCTATATTTTCTAATATGATGATCAATGAGTGC 112
 |||||
 17 rcysLysAlaSerGlyGlyThrPheSerSerTyrAlaIleSerTyrPala 34
 113 GTGAGGCCCCGGGCGAGGCGCTGGAATGATGGGTGAGATCTTACCGGGC 162
 |||||
 34 rglInAlaProGlyGlnGlyLeuGlnIurPmetGlyArgIleIleProIle 50
 163 TCTGTAGACGCGAATATACGAAATTTTAAAGACGCTGTACTATGAC 212
 |||||
 51 LeuGlyIylLeuAlaSnTyrAlaGlnLysPheGlnIylAlaTyrIleTh 67
 213 GCCTGACACTTCGATGATACATGATGACGCTCCAGCTGCAT 262
 |||||

67 ralaAspLysSerThrSerThrAlaTyrMetGluLeuSerSerLeuArgS 84
 263 CGAGAGACACGCGCGCTATATATGCGCGCTATTTTGGCTCTACG 312
 |||||
 84 ecLunSpThrAlaValTyrTyrCysAlaSerSerAsnTyrGly..... 98
 313 CGGAATGGTATTTTATGTTGGGGTCAAGAGACCTGTCTACTGTCTC 362
 99 ProTyrTrpTyrPheAspLeuTyrGlyArgGlyThrLeuValThrVal 115
 363 GAGC 366
 115 rSer 116

seq_name: sp_invertebrate:Q9GYZ2

seq_documentation_block:
 ID Q9GYZ2 PRELIMINARY; PRT: 119 AA.
 AC Q9GYZ2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigoidida; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 OC NCBI_Taxid=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song X.T., Feng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
 RT Schistosoma japonicum";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF282622; AAC01452.1; -.
 FT NON_TER 1
 FT NON_TER 119
 SO SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

alignment_scores:
 Quality: 430.50 Length: 122
 Ratio: 4.100 Gaps: 1
 Percent Similarity: 86.066 Percent Identity: 67.213

alignment_block:
 US-08-487-283A-12_COPY_58_423 x Q9GYZ2 ..

Align seg 1/1 to: Q9GYZ2 from: 1 to: 119

1 CAAGTCAACTGTGTCATCCGCGCGCGAGGTCACAGACCGAGGCGCTC 50
 |||||
 1 GlnValGlnLeuValGlnSerGlyAlaGluValArgLysProGlyLase 17
 51 AGTCAAAGTCTCCTGTAAGCTAGCGGCTATATTTTCTAATATGGA 100
 |||||
 17 rValArgValSerCysLysAlaSerGlyTyrThrPheThnGlyTyrTyrM 34
 101 TTCAAATGGTGGTGCAGCGCGCGGCGAGGCGCTGGAATGAGAGGTGAG 150
 |||||
 34 eLunSpThrAlaValTyrTyrCysAlaSerSerAsnTyrGly..... 50
 151 ATCTTACGCGGCTCTGTAGACACCGAATATACGAAATTTTAAAGACG 200
 |||||
 51 IleAsnProSerArgGlyTyrThrAsnTyrAsnGlnLysPheLysAspAr 67
 201 TGTATCTATGACGCGTACACTTTCGATGATGATGATGATGATGATGAT 250
 |||||
 67 gValThrMetThrThrAspLysSerPheSerThrAlaTyrMetAspLeu 84
 251 CCAAGCTGCGATCGAGACGCGCGCTATATATGCGCGCTTATTTT 300


```

|||||
84 rgSerLeuArgSerAlaaspSerAlaValTyrTyrCysAlaArgTyr 100
301 TTGGTGTACCCGCAATGTTGATGTTGGGTCACGAGCCCT 350
101 .....AspAspHisTyrCysLeuAspTyrTrpGlyGlnGlyThr 114
351 GGTCACTGTCTCGACG 366
|||||
114 rValThrValSerSer 119

```

seq_name: sp_rudent:09Z1C4

seq_documentation_block:
ID 09Z1C4 PRELIMINARY; PRT; 118 AA.

```

AC 09Z1C4;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Mattis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT 16G2/64 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; U78801; AAD0293.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EC559D31EC4FC CRC64;

```

alignment_scores:
Quality: 423.00 Length: 122
Ratio: 4.147 Gaps: 1
Percent Similarity: 83.607 Percent Identity: 63.934

alignment_block:

US-08-487-283A-12_COPY_58_423 x 09Z1C4 ..

Align seg 1/1 to: 09Z1C4 from: 1 to: 118

```

1 CAAGTCCAACGTGTGCAATCCGGCCGAGTCAAGACCAAGGCGCTC 50
|||||
1 GlnValGlnValGlnGlnSerGlyAlaGlnLeuAlaArgProTrpAla 17
17 rValIysLeuSerCysLysAlaSerGlyTyrAsnPheAsnSerTyrTrp 34
51 AGTCAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATATTGA 100
|||||
17 rValIysLeuSerCysLysAlaSerGlyTyrAsnPheAsnSerTyrTrp 34
101 TTCAATGGGTGCGTCAGGCCCCGGGCAAGGCGCTGAATGATGGTGAG 150
|||||
34 eGlnTrpValIysGlnArgProGlyGlnGlyLeuGlnTrpIleGlyAla 50
151 ACTTACCGGGCTGTGTAGCACGCAATATACGAATAATTAAACACG 200
|||||
51 IleTyrProGlyAspGlyAspThrSerTyrTrpGlnLysPheArgGly 67
201 TGTTCATAGACGCGTACACTTCGACATGATGATGATGATGATGAT 250
|||||

```

```

67 sAlaThrLeuThrAlaAspLysSerSerThrAlaTyrIleGlnLeu 84
251 CCAGCTGCGCATCGAGACACGCGCGCTATATTTGCGCGCTATTATT 300
|||||
84 erSerLeuAlaSerGlnAspSerAlaValTyrTyrCysAlaArgThr 100
301 TTGGTGTACCCGCAATGTTGATGTTGGGTCACGAGCCCT 350
|||||
101 ValGlyGly.....TyrPheAspTyrTrpGlyGlnGlyThr 113
351 GGTCACTGTCTCGACG 366
|||||
113 rLeuThrValSerSer 118

```

seq_name: sp_human:095978

seq_documentation_block:
ID 095978 PRELIMINARY; PRT; 157 AA.

```

AC 095978;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE VH1 PROTEIN PRECURSOR (FRAGMENT).
DE VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA Jox A., Zander T., Kuipers R., Irach J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularly Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombined Ig genes.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ005570; CA06599.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT SIGNAL 1
FT SIGNAL 21
FT NON_TER 157
FT NON_TER 157
SQ SEQUENCE 157 AA; 17304 MW; 86986EDA84D88B5 CRC64;

```

alignment_scores:
Quality: 411.50 Length: 122
Ratio: 4.115 Gaps: 1
Percent Similarity: 81.967 Percent Identity: 68.852

alignment_block:

US-08-487-283A-12_COPY_58_423 x 095978 ..

Align seg 1/1 to: 095978 from: 1 to: 157

```

1 CAAGTCCAACGTGTGCAATCCGGCCGAGTCAAGACCAAGGCGCTC 50
|||||
20 GlnValGlnValGlnGlnSerGlyAlaGlnLeuAlaArgProGlyAla 36
51 AGTCAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATATTGA 100
|||||
36 rValIysValHisCysLysThrSerGlyTyrValPheThrSerTyrTrp 53
101 TTCAATGGGTGCGTCAGGCCCCGGGCAAGGCGCTGAATGATGGTGAG 150
|||||
53 LeuIstIrrValArgGlnProArgGlyGlnGlyLeuGlnTrpMetGlyGly 69
|||||

```

```
151 ATCTACCGGGCTGTGGTACGACCGAATATACCGAAATTTTAAAGACCG 200
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
70 ILGLYPRGILYALIGLYSERTHMETCYSLAGILULYSPHEGLNGLYAR 86
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
201 TGTACTATAGACGGCTGACACTTCGACTAGTACAGTATACGAGCCT 250
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
86 GLEUTHMETHTHRAIGSNTHRSERTHRTHRVALTLYRMETGLULEUS 103
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
251 CCAGCCTGCGATCGAGACAGCGCCGCTATATATTCGCCGCTTATTTT 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
103 ERARGLEUARGPHEGLUASPTHRALAVALTYPHECYSGLYARGGLYGLY 119
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
301 TTGGTTCCTAGCCCGAATGGTATTTGGGCTTGCGGCTCAAGACCCCT 350
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
120 ARGTRPARGSEIGLYASN...TYASNGLYHISTPGLYGLNGLYTHPR 135
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
351 GGTCACTGTCTCGAGC 366
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
135 OVALTHRVALSER 140
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

seq_name: sp_human:09Y298

seq_documentation_block:

PRELIMINARY; PRT; 150 AA.

```
ID 09Y298 PRELIMINARY; PRT; 150 AA.
AC 09Y298:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
CC -! SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL; AJ224083; CAAL1829.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR SIGNAL.
KW SIGNAL.
FT NON_TER 1 19 POTENTIAL.
FT SEQUENCE 150 AA; 16031 MW; 563D164AB2280ZD5 CRC64;
```

alignment_scores:

Quality:	394.50	Length:	122
Ratio:	3.830	Gaps:	2
Percent Similarity:	84.426	Percent Identity:	65.574

alignment_block:

US-08-487-283A-12_COPY_58_423 x 09Y298 ..

Align seg 1/1 to: 09Y298 from: 1 to: 150

```
1 CAAGTCCAACTGGTGCATCCGGCGGCGAGTCAAGACGAGCGGCGCTC 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
20 GILVALGILNLEUVALGINSERGLYALAGLIVALLYSLYSPROGLYALASE 36
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
51 AGTCAAGTGTCTGTAAAGTACGAGGCTATATTTTCTAATATTGGA 100
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
36 VALYSVALSERCYSLYSVALSERGLYTYRTHLEUTHRCILUENUPROV 53
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

```
101 TTCATGGGTGCGTCAAGCCCCCGGCGAGGCGCTGGAATGAGGGGTGAG 150
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
53 ALHISTPRVALIGLYNALAPROGLYLSGLYLEUENLUTPRVALGILYSE 69
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
151 ATCTACCGGGCTGTGGTACGACCGAATATACCGAAATTTTAAAGACCG 200
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
70 PHEASPRGILUSERGLYGLUSERTLLETYRVALAARGILUENGLINLYSE 86
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
201 TGTACTATAGACCGCTGACACTTCGACTAGTACAGTATACATGAGCCT 250
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
86 RVALTHRMETHTHRAIASPTHRASPTHRASPLEALATYRMETGLULEUS 103
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
251 CCAGCCTGCGATCGAGACAGCGCCGCTATATATTCGCCGCTTATTTT 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
103 ERSEUARGSERASPSAPTRHVALAVALTYPHYCYSLA..... 116
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
301 TTGGTTCAGCCCGAATGGTATTTGATGTTGGGCTCAAGAACCCCT 350
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
117 ...VALPROASPRGASP...ALAPHEASPILETTPGLYGLNGLYTHME 131
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
351 GGTCACTGTCTCGAGC 366
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
131 VALTHRVALSER 136
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

seq_name: sp_rodent:09QXF0

seq_documentation_block:

PRELIMINARY; PRT; 117 AA.

```
ID 09QXF0 PRELIMINARY; PRT; 117 AA.
AC 09QXF0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 117
FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;
```

alignment_scores:

Quality:	389.50	Length:	122
Ratio:	3.745	Gaps:	1
Percent Similarity:	85.246	Percent Identity:	58.197

alignment_block:

US-08-487-283A-12_COPY_58_423 x 09QXF0 ..

Align seg 1/1 to: 09QXF0 from: 1 to: 117

```
1 CAAGTCCAACTGGTGCATCCGGCGGCGAGTCAAGACGAGCGGCGCTC 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1 GILVALGILNLEUVALGINSERGLYPROGLULEUVALYSLYSPROGLYALASE 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
51 AGTCAAGTGTCTGTAAAGTACGAGGCTATATTTTCTAATATTGGA 100
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
17 VALYSMETSERCYSLYSVALSERGLYTYRTHRPHASPTLYRTYM 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
101 TTCATGGGTGCGTCAAGCCCCCGGCGAGGCGCTGGAATGAGGGGTGAG 150
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
34 ELUYSTRVALYSGLINSERHISGLYLSERLEUENLUTPRILEGILYASP 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
```

```

151 ACTTACCGGGCTGTGTAGCAGCCAAATTACGAAATTTTAAAGACCG 200
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 250
51 IleaapProAsnAsnglyGlyThrserYrAsnglnlySpheylGlyly 67
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 117
67 salathrLeuthrValAspLysSerSerSerthrAlaYrmetGlnLeuA 84
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 134
251 CCAGCGCTCGATCGAGGACAGCGCGCTATATTATGCGCGCGTATT 300
snterLeuthrserGlnspSerAlaValYrYrCysAlaArg..... 350
84 TTTGGTGTATGCCCCGAATGTGATTATTTGTTGGGGTCAAGAACCT 350
99 .....AspLysAspPtyrYrThrAspPtyrTrpGlyGlnGlyThr 112
351 GGTCACCTGCTCGACG 366
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 400
112 lleuthrValserSer 117

seq_name: sp.rodent:09QX99

seq_documentation_block:
ID 09QX99 PRELIMINARY; PRT; 117 AA.
AC 09QX99;
DT 01-MAY-2000 (TREMBLrel, 13, Created)
DT 01-MAY-2000 (TREMBLrel, 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel, 16, last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ225174; CAB55237.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003596; -
DR Pfam; PFO0047; 1q; 1.
DR SMART; SM00406; 1q; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF94D49734 CRC64;

```

```

alignment_scores:
    Quality: 373.50
    Ratio: 3.662
    Percent Similarity: 83.607
    Percent Identity: 57.377
    Length: 122
    Gaps: 1
    alignment_block:
        US-08-487-283A-12_COPY_58_423 x Q9QXE9 ..
        Align seg 1/1 to: Q9QXE9 from: 1 to: 117
        1 CAAGTCACAATGCTTCATCCGGCCGAGCCAGCAAGCCAGGGGCGCTC 50
          ::::::::::: ||::::: ||::: ||::::: ||:::
        1 GUAVALGInLeuGInSerClyProGluLeuValLysProGlyAlaIse 17
          ::::::::::: ||::::: ||::: ||::::: ||:::
        51 AGTCAAGCTGTCCTGTAAGCTAGCGGCTATATTTTCTAATTAATGGA 100
          ::::::::::: ||::::: ||::: ||::::: ||:::
        17 rAllylsmetsrCylsYAlaSerGlyTyrThrPhehrAspIrrYrYim 34
          ::::::::::: ||::::: ||::: ||::::: ||:::
        101 TTCAATGGGTGCGTAGGCCCCGGGGCAGGGCCTTGAAATGATGGGTAG 150
          ::::::::::: ||::::: ||::: ||::::: ||:::
        34 eLysTyrValLysGInSerhIsrLysGlyLysSerLeuGInLTrpIleGlyAsp 50
          ::::::::::: ||::::: ||::: ||::::: ||:::
        151 AACTTACGGGGCTGTGTAGACCCGCAATATACCGAAATTTTAAAGACCG 200
          ::::::::::: ||::::: ||::: ||::::: ||:::
        51 IleAsnProhAsnGlyGlyThrSerTyrAsnGInLysPheLysGly 67

```

```

201  TGTACATCGACGGGTGGACACTGACATGACATGACATGACACTCT 250
    :
    :
    :
67  SAAThtleuthrValSplysSerSerThrAlaTyrmelGlnLeu 84
    :
    :
    :
251  CCAGCTCGCATCGACGAGACAGCCGCTATTATTCGCCGCTTATT 300
    :
    :
    :
84  snserleuthrSerGlnspserAlaValTyrTyrCysAlaArgaspArg 100
    :
    :
    :
301  TTTGGTCTTACCCCGAATTGGATTGATTGTTGGGGTCACAGAACCT 350
    :
    :
    :
101  Tyr.....TyrAlamelaspTyrTpgLglnIyThrse 112
    :
    :
    :
351  GGTCACGTCTCGACG 366
    :
    :
    :
112  rValThrValSerSer 117

```

seq_documentation_block:		PRT; 114 AA.	
ID	09JL81		
AC	09JL81;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	ANTI-MYOSIN IMMUNOGLIBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C;		
RA	Malkiel S., Liao L., Cunningham M.W., Diamond B.;		
RT	"Characterization of cross-reactive monoclonal anti-myosin/anti-n-		
RT	acetyl-glucosamine antibodies from mice with autoimmune myocarditis."		
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF206025; AAF69323.1; -.		
DR	InterPro; IPR003006; -.		
DR	InterPro; IPR003596; -.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
FT	NON_TER 1		
FT	NON_TER 114 114		
SQ	SEQUENCE 114 AA; 12829 MW; 404885FDE6A56F8 CRC64;		

```

alignment_scores:
  Quality: 373.00      Length: 113
  Ratio: 3.885      Gaps: 0
  Percent Similarity: 84.956      Percent Identity: 59.292

alignment_block:
US-08-487-283A-12_COPY_58_423 x Q9JL81 ..

Align seg 1/1 to: Q9JL81 from: 1 to: 114

28 GAGGTCAAGAACCCAGGGGCTCACTCAAAAGTGTCCGTAAAGCTAAGCG 77
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
2  GlnleuValargProGlyAlaIserValIleSerCysIysAlaSerGI 18

78 CTATATTTTCTATATATTGGATTCMAATGGGTGCTCAGAGCCCCGGGGC 127
   ||||  ||:::  ||:::  ||:::  ||:::  ||:::  ||:::  ||:::  ||:::  ||:::
18 yTyrSerPheThrSerTyrTrpMetCHisTrpValIysGlnArgProGIy 35

128 AGGGCCCTGGAATGGATGGGTGAGATCTTAACCGGGGCTGGTATACACGAA 177
   ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
35 lngIySerGluTrpIleGIyMetIleAspProSerGersperGIuTrnArg 51

178 TATACCAAAATTTTAAAGACCGGTGTAATAGACCGTCGACACTTCGAC 227
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
52 LeuAsnGlnIySPheIyAspIyAlaTrnIleuTrnValAspIySerse 68

228 TAGTACGATATACATGAGAGCTCTCCAGGCTGCGATCGAGAGACGACCG 277

```

```

68  rsetThrlaInrymetGlnLeuSerSerProthrSerGluASPSeRAlav 85
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
278 TCATATATGCGCGCGGTATTTTGTGCTAGCCCGAATGGTATTTT 327
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
85  alyrTYrCYsAlArGserasnTYrTYrGlySerSerLeuTYrTYrPhe 101
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
328 GATGTTGGGGTCAAAGAAACCTGGTCACCTGCTGAGC 366
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
102 AspTYrTrpGlyGlnGlyThrlLeuThraValSer 114
      ::::::::::::::::::::::::::::::::::::::::::::::::::::

```

```

seq_name: sp_rudent:Q9QXF0
seq_documentation block:
ID   Q9QXF0      PRELIMINARY;          PRT:   298 AA.
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   CN 8 SCFV.
CN   8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN-BALB/C; TISSUE=SPLEEN;
RA   Shiohara N., Demura T., Fukuda H.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN-BALB/C; TISSUE=SPLEEN;
RA   Shiohara N., Demura T., Fukuda H.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN-BALB/C; TISSUE=SPLEEN;
RA   Shiohara N., Demura T., Fukuda H.;
RT   "Isolation of a novel type of vascular cell wall-specific monoclonal
RT   antibody recognizing a cell polarity using a phage display subtraction
RT   method."
RL   Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR   EMBL: AB036341; BAF86633.1; -.
DR   HSSP: P01607; IREI.
DR   InterPro: IPR003006; -.
DR   InterPro: IPR003596; -.
DR   Pfam: PF00047; Ig: 2.
DR   SMART: SM00406; IGV: 1.
DR   SMART: SM00406; IGV: 1.
SQ   SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

```

```

alignment_scores:
Quality: 359.00      Length: 123
Ratio: 3.626        Gaps: 2
Percent Similarity: 80.488      Percent Identity: 55.285

```

```

alignment_block:
US-08-487-283A-12_COPY_58_423 x Q9QXF0 ..

```

```

Align seg 1/1 to: Q9QXF0 from: 1 to: 298

```

```

1  CAAGTCAAGTGGTCAATCCGCGCCGAGGTCAAGACCGAGGCGCTC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
40  GlnValLysLeuGlnInserGlyGlyLeuValLysProGlyGlyLys 56
51  AGTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTATATTTGCA 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56  rleuYrLysLeuSerGlyAlaAlaSerGlySerAspSerArgYrTrpM 73
101  TTCAATGGGTGCTGACGGCCCGGCGGCTGGAATGGGTGAG 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
73  eSerTrpAlaArgGlnAlaProGlyLysGlyLeuTrpIleGlyGln 89
151  ATCTACCGGGCTGTGTAACACCAATATACGAAATTTTAAAGACG 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
90  IleAnpProAspSerSerThrIleAsnYrThrProSerLeuLysAsp 106
201  TGTACTGTACGCGTGAACCTTGACCTAGTACGATATACATGAGCTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
106  sPheIleLeuSerArgAspAsnAlaLysAsnThrLeuYrLeuGlnMet 123
251  CCAGCGTGGATCGAGACGAGCGCGCTATATTTGCGCGCT...TAT 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123  eYrLysValArgSerGlnAspThrAlaLeuYrYrCysAlaArgAlaSer 139
298  TTTTGTGGTTGTAGCCGCAATGATATTGTTGAGTTGGGTCACGAGAC 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

140  TyrTrpGlyHisSerAla.....TyrTrpGlyGlnGlyTrh 151
348  CCTGGTCACGTCTCGAGC 366
151  rThrValThrValSerSer 157
seq_name: sp_rudent:Q9JL75
seq_documentation block:
ID   Q9JL75      PRELIMINARY;          PRT:   109 AA.
AC   Q9JL75;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN-BALB/C;
RA   Malxiet S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL   Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR   EMBL: AF206031; AAF69329.1; -.
DR   InterPro: IPR003006; -.
DR   InterPro: IPR003596; -.
DR   Pfam: PF00047; Ig: 1.
DR   SMART: SM00406; IGV: 1.
DR   NON_TER 1
FT   NON_TER 109 109
SQ   SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

```

```

alignment_scores:
Quality: 356.00      Length: 114
Ratio: 3.870        Gaps: 2
Percent Similarity: 80.702      Percent Identity: 61.404

```

```

alignment_block:
US-08-487-283A-12_COPY_58_423 x Q9JL75 ..

```

```

Align seg 1/1 to: Q9JL75 from: 1 to: 109

```

```

28  GAGGTCAAGAACCGAGGCGCTCACTCAAGTGTCTGTAAGCTAGCGG 77
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1  GlnLeuValLysProGlyAlaSerValLysMetSerCysLysAlaSerG 17
78  CTATATTTTCTAATATTTGATTCATGAGGTGCGTCAGGCCCGGGGC 127
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  yYrTrhPheThrSerYrValMetHisTrpValLysGlnLysProGlyG 34
128  AGGCGTGAATGATGGGTGAGATCTTACCGGCGCTGTCGATGACCGAA 177
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34  lngLysLeuGlnTrpIleGlyYrIleAsnProYrAsnAspGlyThrLys 50
178  TATACGAAATTTTAAAGACCGTGTACTATGACGGGTGACTTCGAC 227
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  TyrAsnGlnLysPheLysGlyLysAlaThrLeuThrSerAspLysSer 67
228  TAGTACAGTATACATGAGCTCTCCAGCGCTCGATCGAGACAGCGCG 277
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  rSerThrAlaYrMetGlnLeuSerSerLeuThrSerGlnAspSerAla 84
278  TCTATTTGGCGCGCTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 324
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84  alYrYrCysAlaArg.....AspGlyAsnYrYrArgGly 95
325  TTTGATGTTGGGGTCAAGAACCGTGTCACTGTCTCGAGC 366
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96  PheAspYrTrpGlyGlnGlyThrThrLeuThrValSerSer 109

```


OM of: US-08-487-283A-12_COPY_58_423 to: A_Geneseq_0601.* out_format : pfs
Date: Jul 19, 2001 7:54 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framed_nzp.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool/US08487283/runat.19072001_075203_141/app-query.fasta_1.444
-DB=A_Geneseq_0601 -QFMT=fastan -SUFFIX=tra.rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000
-GCAPOP=4.500 -GCAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FCAPOP=6.000 -FCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blissum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MILEN=0 -MAXLEN=200000000
-USER=US08487283.ecgn1_1_85 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLIPX
-WAIT -THREADS=1

Search information block:

Query: US-08-487-283A-12_COPY_58_423
Query length: 366
Database: A_Geneseq_0601.*
Database sequences: 412676
Database length: 60623988
Search time (sec): 38.370000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation	1	3e-63	248	1
/SID8/gcgdata/geneseq/geneseq/AA1995.DAT:AA77607				652.00	1276.37	1.3e-63	248	1	
/SID8/gcgdata/geneseq/geneseq/AA1995.DAT:AA77611				652.00	1276.33	1.3e-63	249	1	
/SID8/gcgdata/geneseq/geneseq/AA1995.DAT:AA77615				627.00	1226.93	7.5e-61	249	1	
/SID8/gcgdata/geneseq/geneseq/AA1995.DAT:AA77616				623.00	1219.06	2.1e-60	248	1	
/SID8/gcgdata/geneseq/geneseq/AA1995.DAT:AA77610				617.00	1207.17	9.4e-60	249	1	
/SID8/gcgdata/geneseq/geneseq/AA1995.DAT:AA77606				555.00	1084.67	6.3e-53	248	1	
/SID8/gcgdata/geneseq/geneseq/AA1995.DAT:AA77609				514.50	1084.64	6.3e-53	249	1	
/SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAW90936				515.00	998.81	2.0e-48	470	1	
/SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAW90935				503.50	977.07	3.3e-47	470	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62209				502.00	985.22	3.9e-47	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62217				502.00	985.22	3.9e-47	139	1	
/SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAW90933				500.50	971.14	7.0e-47	470	1	
/SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAW90934				499.50	969.16	9.0e-47	470	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62210				499.00	979.29	8.3e-47	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02556				499.00	979.29	8.3e-47	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62204				498.00	977.31	1.1e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02570				498.00	977.31	1.1e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02571				498.00	977.31	1.1e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW83037				497.50	965.21	1.5e-46	470	1	
/SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAW14779				497.50	965.21	1.5e-46	470	1	
/SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAW90929				497.50	965.21	1.5e-46	470	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62217				497.00	975.33	1.4e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02561				497.00	975.33	1.4e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62211				496.00	973.36	1.8e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02557				496.00	973.36	1.8e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62213				495.00	971.38	2.3e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02559				495.00	971.38	2.3e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAV02572				493.50	963.25	3.7e-46	245	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62212				493.00	967.43	3.8e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02558				493.00	967.43	3.8e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW65773				492.00	965.45	4.9e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62205				492.00	965.45	4.9e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV32770				492.00	965.45	4.9e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02572				492.00	965.45	4.9e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02576				492.00	965.45	4.9e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAV7294				491.00	965.39	6.3e-46	140	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAW62196				491.00	963.48	6.3e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02562				491.00	963.48	6.3e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62218				490.00	961.50	8.2e-46	139	1	
/SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAV70603				489.50	961.70	9.0e-46	122	1	

/SID8/gcgdata/geneseq/geneseq/AA1994.DAT:AAW50188	+	489.50	960.32	9.3e-46	142
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV26984	+	489.50	960.32	9.3e-46	142
/SID8/gcgdata/geneseq/geneseq/AA1992.DAT:AAW22421	+	489.00	961.02	1.0e-45	118
/SID8/gcgdata/geneseq/geneseq/AA1994.DAT:AAW54758	+	489.00	961.02	1.0e-45	118
/SID8/gcgdata/geneseq/geneseq/AA1999.DAT:AAV26986	+	488.50	958.34	1.2e-45	142

seq.name: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT:AA77607

seq_documentation_block:

ID AAR77607 standard; Protein: 248 AA.
AC AAR77607;
DT 15-MAR-1996 (first entry)
DE Humanised CDR-grafted 5G1.1 scFv CB.
XX
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarily determining region; CDR;
KW single chain antibody; scFv.

Synthetic.

Key	Location/Qualifiers
Region	26..36
Region	/label= CDR-L1
Region	52..58
Region	/label= CDR-L2
Region	91..99
Region	/label= CDR-L3
Region	152..161
Region	/label= CDR-H1
Region	176..192
Region	/label= CDR-H2
Region	225..237
Region	/label= CDR-H3

WC9529697-A1.

09-NOV-1995.

01-MAY-1995; 95WC-U505688.

02-MAY-1994; 94US-0236208.

(ALEX-) ALEXION PHARM INC.

Evans MJ, Matls L, Mueller EE, Nye SH, Rollins S;

Rother RP, Springhorn J P, Squinto SP, Thomas TC;

Wang Y, Wilkins JA;

WPI: 1995-392923/50.

N-PSDB; AAT08480.

Treating glomerulonephritis with antibody against complement C5

component - to inhibit complement induced cell lysis

Example 11; Page 110-113; 181pp; English.

Humanised CDR-grafted 5G1.1 scFv CB (AAR77607) is the product of a
DNA construct (AAT08479) derived from DNA of hybridoma ATCC HB 11625,
the producer of anti-C5 monoclonal antibody (MAb) 5G1.1. Recombinant
scFv CB is obtd. by expression of this DNA in Escherichia coli using
vector pET T1c SO5/NT. The light and/or heavy chain CDRs of
scFv CB can be combined with CDRs from other 5G1.1-derived antibodies,
Fcs and light chains (AAR77606-16) in the prodn. Of recombinant,
including humanised, antibodies that retain the ability of MAb 5G1.1
to block human complement C5a generation and thus to reduce glomerular
inflammation and kidney dysfunction associated with glomerulonephritis.

Sequence 248 AA:

alignment_scores:

Quality: 652.00 Length: 122
Ratio: 5.344 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAR77607 ..

Align seg 1/1 to: AAR77607 from: 1 to: 248

```
1 CAATGCCACTGCTGCAATCCGGCCGCAAGAACCCAGGGGCTCT 50
|||||
127 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe 143
51 AGTCAAGTCTGCTGTAAGCAGCGGCTAATTTTCTAATTTTGA 100
|||||
143 rValLysValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrpI 160
101 TTCAATGGGTCGTCAGACCCCGGGCAGGGCTGGAATGATGGGTAG 150
|||||
160 legIntPrValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGlu 176
151 ATCTTACCGGGCTCTGGTAGACCGAATATACCGAAATTTTAAAGACCG 200
|||||
177 IleuProGlySerGlySerThrGluTyrThrGluAsnPhelyAspAr 193
201 TGTACTATGACGGCTGACACTGCTAGTACATACATACATAGAGCTCT 250
|||||
193 gValThrMetThrArgAspTrpThrSerThrValTyrMetGluLeuS 210
251 CCAGCTTCGATCGAGAGACACGCGCTATATTATTCGCGCGTATTATT 300
|||||
210 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgTyrPhe 226
301 TTTCGTTCTAGCCCGCAATGTGATTTTGTGTTGGGCTCAAGAACCTC 350
|||||
227 PheGlySerSerProAsnTyrPyrPheAspValTrpGlyGlnGlyThrLe 243
351 GGTCACTGCTCGAGC 366
|||||
243 uValThrValSerSer 248
```

seq_name: /SID8/gcgdata/geneseq/geneseqp/AA1995.DAT: AAR77611

seq_documentation_block:

ID AAR77611 standard; Protein: 249 AA.

XX AAR77611;

DT 02-APR-1996 (first entry)

XX Humanised 561.1 VH + IGHRLC.

XX Complement C5; haemolysis; kidney; glomerulonephritis;

KW monoclonal antibody; antiinflammatory; antibody engineering;

XX humanised antibody; complementarity determining region; CDR.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19 /label= sig_peptide

FT Peptide 20..249 /label= mat_peptide

XX W09529697-A1.

XX 09-NOV-1995.

XX 01-MAY-1995; 95WO-US05688.

XX 02-MAY-1994; 94US-0236208.

XX (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

XX WPI: 1995-392923/50.

XX DR N-PSDB: AAT08484.

XX Treating glomerulonephritis with antibody against complement C5

PT component - to inhibit complement induced cell lysis

XX Claim 38; Page 123-125; 181pp; English.

XX A DNA construct (AAT08483) codes for a humanised CDR-grafted and

CC framework sequence-altered Fd 561.1 VH + IGHRL (AAR77610), which

CC includes CDRs derived from mouse anti-C5 monoclonal antibody 561.1.

CC The DNA can be subcloned together with DNA (AAT08484) coding for a

CC humanised light chain (AAR77612) into vector APEX-3P (AAT08476) for

CC expression of humanised antibody in human 293 EBNA cells. Such

CC recombinant antibodies retain the ability of Mab 561.1 to block

CC human complement C5a generation and thus to reduce glomerular

CC inflammation and kidney dysfunction associated with

CC glomerulonephritis.

CC Sequence 249 AA:

alignment_scores:

Quality: 652.00 Length: 122
Ratio: 5.344 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAR77611 ..

Align seg 1/1 to: AAR77611 from: 1 to: 249

```
1 CAAGTCCACTGCTGCAATCCGGCCGAGGTCAAGAACCCAGGGGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe 36
51 AGTCAAGTCTGCTGTAAGCAGCGGCTAATTTTCTAATTTTGA 100
|||||
36 rValLysValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrpI 53
101 TTCAATGGGTCGCTCAGACCCCGGGCAGGGCTGGAATGATGGGTAG 150
|||||
53 legIntPrValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGlu 69
151 ATCTTACCGGGCTCTGGTAGACCGAATATACCGAAATTTTAAAGACCG 200
|||||
70 IleuProGlySerGlySerThrGluTyrThrGluAsnPhelyAspAr 86
201 TGTACTATGACGGCTGACACTTCTAGTACATACATACATAGAGCTCT 250
|||||
86 gValThrMetThrArgAspTrpThrSerThrValTyrMetGluLeuS 103
251 CCAGCTTCGATCGAGAGACACGCGCTATATTATTCGCGCGTATTATT 300
|||||
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgTyrPhe 119
301 TTTCGTTCTAGCCCGCAATGTGATTTTGTGTTGGGCTCAAGAACCTC 350
|||||
120 PheGlySerSerProAsnTyrPyrPheAspValTrpGlyGlnGlyThrLe 136
351 GGTCACTGCTCGAGC 366
|||||
136 uValThrValSerSer 141
```

seq_name: /SID8/gcgdata/geneseq/geneseqp/AA1995.DAT: AAR77615


```
seq_documentation block:
ID AAR77615 standard; Protein: 249 AA.
XX
AC AAR77615;
XX
DT 02-APR-1996 (first entry)
XX
DE Humanised 5G1.1 VH + IGHRLD.
XX
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig_peptide
FT Peptide 20..249
FT /label= mat_peptide
XX
PN MO9529697-A1.
XX
PD 09-NOV-1995.
XX
PF 01-MAY-1995; 95WO-US05688.
XX
PR 02-MAY-1994; 94US-0236208.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
XX
DR MPI: 1995-392923/50.
DR N-PSDB: AAT08487.
XX
PT Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
XX
PS Claim 37; Pages 135-137; 181pp; English.
XX
CC A DNA construct (AAT08487) codes for a humanised CDR-grafted
CC light chain, designated 5G1.1 VL + IGHRLD (AAR77615), which includes
CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
CC DNA can be subcloned together with DNA (AAT08484) coding
CC for a humanised Fd (AAR77611) into vector APEX-3P (AAT08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of MAb 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
XX
SQ Sequence 249 AA;
```

```
alignment_scores:
Quality: 627.00 Length: 122
Ratio: 5.182 Gaps: 0
Percent Similarity: 99.180 Percent Identity: 95.902
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alignment_block:

US-08-487-283A-12_COPY_58_423 x AAR77615 ..

Align seg 1/1 to: AAR77615 from: 1 to: 249

```
1 CAAGTCCAACTGGTGCATTCGGCGCCAGGTCAAGAAGCCAGGCGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysLysProGlyAlaSe 36
51 AGTCAAGTCTCTGTAAGCTAGCGGCTATATTTTTCATAATTATGGA 100
|||||
```

```
36 rValLysValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrpI 53
101 TTCATGGGTGGTCAGGCCCCCGGCGAGCCCTGGATGATGATGGTGAG 150
|||||
53 IeGlnTrpValArgGlnAlaProGlyGlnGlyLeuGlnLutPheMetGlyL 69
151 ATCTTACCGGCTCTGGTAGCACCGAATATACCGAAATTTTAAACCG 200
|||||
70 IleLeuProGlySerGlySerThrGlnTyrAlaGlnLysPheGlnGly 86
201 TGTCTATGACGCGGTGACACTTCGACTGTACAGTATCATGACGCTCT 250
|||||
86 gValIleThrMetThrArgAspThrSerThrSerThrValTyrMetGlnLeu 103
251 CCAGCCTGGATCGAGACAGCGCGCTCTATTATGCGCGCTTATTTT 300
|||||
103 erSerLeuArgSerGlnAspThrAlaValTyrCysAlaArgTyrPhe 119
301 TTGGGTTCTAGCCCGAATTTGATTTTGATGTTTGGGGTCAGAACCT 350
|||||
120 PheGlySerSerProAsnTrpTyrPheAspValTrpGlyGlnGlyThr 136
351 GGTCACGTGCTCGAGC 366
|||||
136 vValThrValSerSer 141
seq_name: /SID58/gcgdata/geneseq/geneseq/A11995.DAT: AAR77615
seq_documentation block:
ID AAR77616 standard; Protein: 248 AA.
XX
AC AAR77616;
XX
DT 15-MAR-1996 (first entry)
XX
DE Humanised CDR-grafted 5G1.1 scFv DO12.
XX
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW single chain antibody; scFv.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 26..36
FT /label= CDR-L1
FT Region 52..58
FT /label= CDR-L2
FT Region 91..99
FT /label= CDR-L3
FT Region 152..161
FT /label= CDR-H1
FT Region 176..186
FT /label= CDR-H2
FT Region 225..237
FT /label= CDR-H3
XX
PN MO9529697-A1.
XX
PD 09-NOV-1995.
XX
PF 01-MAY-1995; 95WO-US05688.
XX
PR 02-MAY-1994; 94US-0236208.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
XX
DR MPI: 1995-392923/50.
```

DR N-PSDB; AAT08488.
 XX Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 XX
 PS Example 11; Page 138-140; 181pp; English.
 XX
 CC A humanised CDR-grafted scFv, designated 5G1.1 scFV D012 (AAR77616),
 CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
 CC The scFv can be expressed in Escherichia coli ME1 cells by subcloning
 CC of encoding DNA (AAT08488) into vector pET T1c S05/N1. This 5G1.1 to
 CC humanised, recombinant antibody retained the ability of Mab 5G1.1 to
 CC block human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 CC
 XX
 SQ Sequence 248 AA:

alignment_scores:
 Quality: 623.00 Length: 122
 Ratio: 5.149 Gaps: 0
 Percent Similarity: 99.180 Percent Identity: 95.082

alignment_block:
 US-08-487-283A-12_COPY_58_423 x AAR77616 ..

Align seg 1/1 to: AAR77616 from: 1 to: 248

```

1 CAAGTCCAACTGGTGCAATCCGGCCGAGGTCAAGAACCGAGGCGCTC 50
  |||
127 GlnValGlnLeuValGlnSerGlyAlaGlnValGlnLysProGlyAla 143
  |||
51 AGTCAAAATGTCCTTAAGCTAGCGGCTATTTTCTATATATGCA 100
  |||
143 rVallyValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrp 160
  |||
101 TTCATGGGTCGTCAGAGCCCGGCGAGGCGCTGAATGATGGGTGAG 150
  |||
160 LegIntPrValArgGlnAlaProGlyGlnGlyLeuGlnTyrPmetGlyGlu 176
  |||
151 ATCTTACCGGCTCTGTAGACACGCAATATACGAAATTTTAAAGACCG 200
  |||
177 IleuProGlySerGlySerThrGlnTyrAlaGlnLysPheGlnGlyLys 193
  |||
201 TGTAATCTGACGGGTGACACTGTGACAGTATGATATCATGAGGCTCT 250
  |||
193 gValThrMetThrArgAspTrpSerThrSerThrValTyrMetGlnLeu 210
  |||
251 CCAGCTTCGATCGAGGACACGCGCTATATTGCGCGGCTATTTT 300
  |||
210 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgTyrPhe 226
  |||
301 TTGGTCTAGCCCGCAATGTGATTGTTGGGTCAAGAACCGCT 350
  |||
227 PheGlySerSerProAsnTrpTyrPheAspValTyrGlyGlnGlyThr 243
  |||
351 GGTCACTGCTCTCGAGC 366
  |||
243 uValThrValSerSer 248
  |||

```

seq_name: /SIDS98/gcgdata/geneseq/geneseq/AA1995.DAT: AAR77610
 seq_documentation_block:
 ID AAR77610 standard; Protein: 249 AA.
 XX AAR77610;
 AC
 XX
 XX
 DT 15-MAR-1996 (first entry)
 XX
 DE Humanised 5G1.1 VH + IGHRL.
 XX
 XX Complement c5; haemolysis; kidney; glomerulonephritis;

KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT 20..249
 FT /label= mat_peptide
 FT 45..54
 FT Region /label= CDR-H1
 FT 69..79
 FT Region /label= CDR-H2
 FT 118..130
 FT Region /label= CDR-H3
 FT
 PN W09529697-A1.
 XX
 XX
 PD 09-NOV-1995.
 XX
 PF 01-MAY-1995; 95MO-US05688.
 XX
 PR 02-MAY-1994; 94US-0236208.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matlis L, Mueller EF, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR WPI: 1995-392923/50.
 DR N-PSDB; AAT08483.
 XX
 XX Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 XX
 XX
 PS Example 11; Page 119-122; 181pp; English.

alignment_scores:
 Quality: 617.00 Length: 122
 Ratio: 5.142 Gaps: 0
 Percent Similarity: 98.361 Percent Identity: 94.262

alignment_block:
 US-08-487-283A-12_COPY_58_423 x AAR77610 ..

Align seg 1/1 to: AAR77610 from: 1 to: 249

```

1 CAAGTCCAACTGGTGCAATCCGGCCGAGGTCAAGAACCGAGGCGCTC 50
  |||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValGlnLysProGlyAla 36
  |||
51 AGTCAAAATGTCCTTAAGCTAGCGGCTATTTTCTATATATGCA 100
  |||
36 rVallyValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrp 53
  |||
101 TTCATGGGTCGTCAGAGCCCGGCGAGGCGCTGAATGATGGGTGAG 150
  |||
53 LegIntPrValArgGlnAlaProGlyGlnGlyLeuGlnTyrPmetGlyGlu 69
  |||

```

A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH + IGHRL (AAR77610), includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. It can be co-expressed with a humanised light chain (AAR77612) in human 293 EBNA cells using encoding DNAs subcloned into vector ALEX-3P (AAT08476). Such humanised recombinant antibodies retain the ability of Mab 5G1.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.

```

151 ATCTACCGGCTCTGTGACACGAAATATACGAAATTTTAAGACCG 200
|||||
70 IleleuproGlySerGlySerThrGluTyrAlaGlnLysPheGlnGlyAr 86
201 TGTACTATGACCGCTGACACTTCGACTAGTACAGTATGACGAGCTCT 250
|||||
86 gValThrMetThrAlaAspThrSerThrSerThrAlaTyrMetClnLus 103
251 CCAGCCTGGATCGAGACACAGCGCCGCTATATATTCGCCGCTATTTT 300
|||||
103 erSerLeuArGSerGluAspThrAlaValTyrTyrCysAlaArgTyrPhe 119
301 TTTGGTTCTAGCCCGAATGTGATTTTGATGTTGGGTCACAGAACCT 350
|||||
120 PheGlySerSerProAsnTrpTyrPheAspValTrpGlyGlnGlyThrLe 136
351 GGTCACTGTCTCGAGC 366
|||||
136 vValThrValSerSer 141

seq_name: /SID58/gcgdata/geneseq/geneseqp/AA1995.DAT:AA77606

seq_documentation_block:
ID AAR7606 standard; Protein: 248 AA.
AC AAR7606;
XX
XX
DT 15-MAR-1996 (first entry)
XX
XX Murine 5G1.1m1 scfv.
XX
XX Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR
XX single chain antibody; scfv.
XX
XX Mus sp.
XX
XX OS
XX
XX Key Location/Qualifiers
FH 28..34
FT Region /Label= CDR-L1
FT 52..54
FT Region /Label= CDR-L2
FT 93..98
FT Region /Label= CDR-L3
FT 156..159
FT Region /Label= CDR-H1
FT 179..183
FT Region /Label= CDR-H2
FT 226..236
FT Region /Label= CDR-H3
FT
XX
XX W09529697-A1.
XX
XX 09-NOV-1995.
XX
XX 01-MAY-1995; 95WO-US05688.
XX
XX 02-MAY-1994; 94US-0236208.
XX
XX (ALEX-) ALEXION PHARM INC.
XX
XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
XX
XX WPI: 1995-392923/50.
XX
XX N-PSDB: AAT08479.
XX
XX
XX Treating glomerulonephritis with antibody against complement C5
XX Component - to inhibit complement induced cell lysis
XX
XX Example 11: Page 107-110; 181pp; English.

```

```

XX
XX Murine scfv 5G1.1m1 (AAR7606) is the product of a DNA construct
CC (AAR08479) obtd. from DNA of hybridoma ATCC HB 11625, which produces
CC anti-C5 monoclonal antibody (Mab) 5G1.1. Recombinant scfv 5G1.1m1 is
CC obtd. by expression of this DNA in Escherichia coli using vector PET
CC Trc S05/NI. The light and/or heavy chain CDRs of scfv 5G1.1m1 can
CC be combined with CDRs from other 5G1.1-derived antibodies, Fds and
CC light chains (AAR7607-16) in the prodn. of recombinant, including
CC humanised, antibodies that retain the ability of Mab 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
XX
XX Sequence 248 AA;
SQ

alignment_scores:
Quality: 555.00 Length: 122
Ratio: 4.826 Gaps: 0
Percent Similarity: 94.262 Percent Identity: 81.148

alignment_block:
US-08-487-283A-12_COPY_58_423 x AAR77606
..
Align seg 1/1 to: AAR77606 from: 1 to: 248

1 CAAGTCCAACTGTGTCATCGGCGCCGAGGTCAAGACGAGCGGCTC 50
|||||
127 GlnValGlnLeuGlnGlnSerGlyAlaGlnLeuMetLysProGlyLysAla 143
51 AGTCAAGTCTCTGTAAGCTAGCGGCTATATTTTCTATATATGGA 100
|||||
143 rValLysMetSerCysLysAlaThrClyTyrIlePheSerAsnTyrTrpI 160
101 TTCATGGGTGGCTCAGCGCCCGGCGAGGCTGGAATGAGTGGCTGAG 150
|||||
160 legInTrpIleLysGlnArGProGlyHisGlyLeuGlnTrpIleGlyGln 176
151 ATCTTACCGGCTCTGTGACACGAAATATACGAAATTTTAAGACCG 200
|||||
177 IleleuproGlySerGlySerThrGluTyrThrGlnAsnPheLysAspLys 193
201 TGTACTATGACCGCTGACACTTCGACTAGTACAGTATGACGAGCTCT 250
|||||
193 sAlaAlaPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLus 210
251 CCAGCCTGGATCGAGACACAGCGCCGCTATATATTCGCCGCTTTT 300
|||||
210 erSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrPhe 226
301 TTTGGTTCTAGCCCGAATGTGATTTTGATGTTGGGTCACAGAACCT 350
|||||
227 PheGlySerSerProAsnTrpTyrPheAspValTrpGlyAlaGlyThrH 243
351 GGTCACTGTCTCGAGC 366
|||||
243 rValThrValSerSer 248

seq_name: /SID58/gcgdata/geneseq/geneseqp/AA1995.DAT:AA77609

seq_documentation_block:
ID AAR77609 standard; Protein: 249 AA.
XX
XX AAR77609;
XX
XX 02-APR-1996 (first entry)
XX
XX Chimeric heavy chain 5G1.1m1 VL HuG1.
XX
XX Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW chimeric antibody; Fab.

```


CC. versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
 CC which is described in the method of the invention.

XX Sequence 470 AA:

alignment_scores: Length: 125
 Quality: 514.50 Gaps: 2
 Ratio: 4.553
 Percent Similarity: 90.400 Percent Identity: 80.000

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAW90936 ..

Align seg 1/1 to: AAW90936 from: 1 to: 470

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1  CAAGTCCAACTGGTGCATCCGGCGGAGGTCAAGAACGAGGGGCGTC 50
  ||||||||||||||||||||||||||||||||||||||||||||||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
  ||||||||||||||||||||||||||||||||||||||||||||||||
51 AGTCAAGTGTCTCTTAAGCTAGCGGCTATATTTTTCATATTTTGA 100
  ||||||||||||||||||||||||||||||||||||||||||||||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrSerTyr 53
  ||||||||||||||||||||||||||||||||||||||||||||||||
101 TTCATGGTGGTGCAGGCCCGGCGGAGGCGCTGAGTGGATGGTGAG 150
  ::::::::::::::::::::::::::::::::::::::::::::::::::::
53 ecIcIntrpValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGly 69
  ||||||||||||||||||||||||||||||||||||||||||||||||
151 ANCTTACGGGGCTCTGTAGCAGCAATNACGAAATTTTAAAGACCG 200
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
70 IleAspProSerAspSerTyrThrAsnTyrAsnGlnLysPheLysGly 86
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
201 TGTATATAGACGCGTACACTTCGACTAGTACGATACATGAGGCTCT 250
  ||||||||||||||||||||||||||||||||||||||||||||||||
86 gValThrIleThrArgAspThrSerThrAlaTyrMeclLueus 103
  ||||||||||||||||||||||||||||||||||||||||||||||||
251 CCAGCGTGGATCGAGACACGCGGCTATATTTGCGGCGCT..... 294
  ||||||||||||||||||||||||||||||||||||||||||||||||
103 exSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgAsn 119
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
295 ...TATTTTTCGTCTAGCCCGAATTTGATTTTGGATTTGGGCTCA 341
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 AspTyr.....SerAsnAsnTrpTyrPheAspValTrpGly 132
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
342 AGGAACCTGTGCATCTCTCGAGC 366
  :||||||||||||||||||||||
132 uGlyThrLeuValThrValSerSer 140
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

seq_name: /SIDS8/gcdata/geneseq/geneseq/AA2000.DAT:AAW90935

seq_documentation_block:

ID AAW90935 standard; Protein: 470 AA.

XX AAW90935:

DT 08-AUG-2000 (first entry)

XX Humanised anti-Fas designed heavy chain Heu 3 protein.

KW Fas: antibody; human: anti-inflammatory; anti-anemic; antidiabetic;
 KM anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;

KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KM nephrotropic; antifertility; neuroprotective; antiatherosclerotic;
 KM hepatocytic; humanized; apoptosis; systemic lupus erythematosus;
 KM Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KM Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KM Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KM multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KM cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Synthetic.
 XX EP990663-A2.
 PN 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 PF 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 PA (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 DR N-PSDB; AAA11646.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 XX Claim 2: Page 180-182; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,
 CC antiatherosclerotic, cardiac and hepatocytic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
 CC which is described in the method of the invention.

SO Sequence 470 AA:

alignment_scores: Length: 125
 Quality: 503.50 Gaps: 2
 Ratio: 4.496
 Percent Similarity: 89.600 Percent Identity: 78.400

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAW90935 ..

Align seg 1/1 to: AAM62209 from: 1 to: 470

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1 CAAGTCCAACTGTGCAATCCGGCCGAGGTCAAGAACCCAGGGCCCTC 50
  |||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysLysProGlyAlaIse 36
  |||
51 AGTCAAGTGTCTGTAAGCTAGCGGCTATATTTCTAATTTATGGA 100
  |||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrSerTyrTrpM 53
  |||
101 TTCATGGGTGGTCAGGCCCCGGGCGCTGGAATGATGGGTGAG 150
  |||
53 eGlnTrpValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGlyGln 69
  |||
151 ATCTTACCGGGCTGTGTAGACCGCAATATACGAAATTTTAAAGACCG 200
  |||
70 IleAspProSerAspSerTyrThrAsnTyrAsnGlnLysPheLysGlyLys 86
  |||
201 TGTATCATGACGCGTGTGACACTTGTGACTAGTACATGATGAGACTCT 250
  |||
86 sAlaThrLeuThrValAspThrSerThrSerThrAlaTyrMetGlnLeuS 103
  |||
251 CCAAGCTGCGATCGAGACAGCGCCGCTATATTTGCGCGCGT..... 294
  |||
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgAsnArg 119
  |||
295 ...TATTTTGTGTTCTAGCCCAATTGGTATTTTGTGATGGGTGCA 341
  |||
120 AspTyr.....SerAsnAsnTrpTyrPheAspValTrpIleGly 132
  |||
342 AGGAACCTGTGCTACTGTCTGAGC 366
  |||
132 nGlyThrLeuValThrValSerSer 140
  |||

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seq_name: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT: AAM62209

seq_documentation_block:

ID AAM62209 standard; Protein; 139 AA.

AC AAM62209;

XX 21-SEP-1998 (first entry)

DT Humanised anti-HM1.24 antibody H chain V region HEF-RVHa-AHM g-gamma-1.

XX Humanised anti-HM1.24 antibody H chain V region HEF-RVHa-AHM g-gamma-1.

XX Mouse; human: humanised: anti-HM1.24 antibody; myeloma; FR; CDR;

KW framework region; complementarity determining region; antigenicity.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

XX W09814580-A1.

XX W09814580-A1.

XX 09-APR-1998.

XX 03-OCT-1997; 97WO-JP03553.

XX 04-OCT-1996; 96JP-0264756.

XX (CHUGAI SEIYAKU KK.

XX Koshihara Y, Kosaka M, Ohtomo T, Ono K, Tsuchiya M;

PI Yoshimura Y;

XX WPI; 1998-286421/25.

DR N-PSDB; AAV39396.

XX Humanised anti-HM1.24 antibody - for treatment of myeloma

PT Example; 9; Page 106-107; 210pp; Japanese.

PS A humanised anti-HM1.24 antibody has been developed which comprises

XX CC

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

CC human L and H chain C regions, and L and/or H chain V regions
 CC containing material originating in mouse anti-HM1.24 antibody. The V
 CC regions contain framework (FR) regions of human origin and
 CC complementarity determining regions (CDR) of mouse origin, leading to
 CC a reshaped humanised antibody. The C regions are human Ck (L-chain) and
 CC human C gamma (especially C gamma 1) (H-chain). The FR regions of the
 CC L chain V region are derived from human subtype Hs61 (e.g. from human
 CC antibody R61) and the FR regions of the H chain V region are derived
 CC from human subtype Hs61 (e.g. FR1-3 from human antibody Hs3 and FR4
 CC from human antibody Hs6). The present sequence represents an H chain
 CC V region from the present invention. The antibodies are used for
 CC the treatment of myeloma, especially by injection, intravenously,
 CC intramuscularly or subcutaneously. The antibodies are used at 0.01-1000
 CC (especially 5-100) mg/kg body weight. The humanised antibody has low
 CC antigenicity and is therefore effective therapeutically in humans.
 CC
 XX
 S0 Sequence 139 AA.

alignment_scores:

Quality: 502.00 Length: 122

Ratio: 4.564 Gaps: 1

Percent Similarity: 90.164 Percent Identity: 79.508

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAM62209 ..

Align seg 1/1 to: AAM62209 from: 1 to: 139

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1 CAAGTCCAACTGTGCAATCCGGCCGAGGTCAAGAACCCAGGGCCCTC 50
  |||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysLysProGlyAlaIse 36
  |||
51 AGTCAAGTGTCTGTAAGCTAGCGGCTATATTTCTAATTTATGGA 100
  |||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrProTyrTrpM 53
  |||
101 TTCATGGGTGGTCAGGCCCCGGGCGCTGGAATGATGGGTGAG 150
  |||
53 eGlnTrpValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGlyGlySer 69
  |||
151 ATCTTACCGGGCTGTGTAGACCGCAATATACGAAATTTTAAAGACCG 200
  |||
70 IlePheProGlyAspGlyAspThrArgTyrSerGlnLysPheLysGlyArg 86
  |||
201 TGTATCATGACGCGTGTGACACTTGTGACTAGTACATGATGAGACTCT 250
  |||
86 gValThrMetThrAlaAspThrSerThrSerThrValTyrMetGlnLeuS 103
  |||
251 CCAAGCTGCGATCGAGACAGCGCCGCTATATTTGCGCGCGTATTTT 300
  |||
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgGlyLeu 119
  |||
301 TTTGGTCTAGCCCAATTGGTATTTGATTTGGGTGCAAGAACCTCT 350
  |||
120 .....ArgArgGlyGlyTyrTyrPheAspTyrTrpGlyGlnGlyThrTh 134
  |||
351 GGTACTGTCTCGAGC 366
  |||
134 rValThrValSerSer 139
  |||

```

seq_name: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT: AAV02555

seq_documentation_block:

ID AAV02555 standard; Protein; 139 AA.

AC AAV02555;

XX 16-JUL-1999 (first entry)

DT Humanised H chain V region of antiHM1.24 antibody.

XX Reconstituted human antibody; peptide antigen HM1.24; framework region;

DE

XX

XX

XX

XX

XX

XX

XX	complementary determining region; CDR, anti-HM1.24 antibody; myeloma;
XX	humanized antibody.
XX	
OS	Synthetic.
OS	Mus sp.
XX	
PN	WO910212-A1.
XX	
PD	15-APR-1999.
XX	
PF	02-OCT-1998; 98WO-JP04469.
XX	
PR	03-OCT-1997; 97JP-0271726.
XX	
PA	(CHUS) CHUGAI SEIYAKU KK.
PI	
XX	Tsuchiya M;
DR	WPI: 1999-277273/23.
XX	
DR	N-P.SDB; AAX36290.
XX	
PT	Reconstituted human antibody useful in the treatment of myeloma
XX	
PS	Disclosure; Page 86-87; 256pp; Japanese.
XX	
CC	The specification describes a reconstituted human antibody recognizing
CC	the peptide antigen HM1.24. This human antibody contains natural human
CC	framework regions modified by amino acid substitutions to provide
CC	homogeneity with a previously designed framework region (which may
CC	arise from a human or non-human source); and complementary determining
CC	regions (CDR) derived from a non-human anti-HM1.24 antibody. The
CC	reconstituted antibody is useful in the treatment of diseases in which
CC	the surface antigen HM1.24 is implicated such as myeloma. The present
CC	sequence is used in the creation of the antibodies of the invention.
CC	

SQ Sequence 139 AA;

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alignment_scores:
  Quality: 503.00
  Ratio: 4.564
  Percent Similarity: 90.164
  Length: 122
  Gaps: 1
  Percent Identity: 79.508
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alignment_block:

US-08-487-283A-12_COPY_58_423 x AAY02555

Align seq 1/1 to: AAY02555 from: 1 to: 139

1 CAAGTCACACAGTGTCGCAATCCGGGCGCCGAGGTCACAGACCGAGGGGCTC 50
20 GlnValGlnLeuValGlnSerGlnValGlnValLysLysProGlyAlaIle 36
51 AGTCAAAGTCGTCCTTAAAGCTACGGGCGCATATTTTTCCTAAATATTGCA 100
36 rValLysValSerCysLysAlaSerGlyThrPheThrProIleTyrPm 53
101 TTCAATGGGTCGTCAGACCCCGGGGACAGGCGCTGAATGATGAGGTGAG 150
53 etGlnTrpValArgGlnAlaProGlyGlnGlyLeuGlnIleTrpMetGlySer 69
151 ATCTTACCGGGCTCTGTAGACACGCAATATACGAAATTTTAAAGACCG 200
70 IlePheProGlyAspGlyAspIlePheArgTyrSerGlnLysPheLysGlyAr 86
201 TGTTACTATGACGCGTGCACACTTCGACTAGTACAGTATACATGAGAGCTCT 250
86 GValThrMetThrAlaAspThrSerThrSerThrValTyrMetGlnLeuS 103
251 CCAGCGTCGCAATCGAGGACGACGGCGCTATATTATGGCGCGCTATATT 300
103 erSerLeuArgSerGlnAspThrAlaValLysTyrCysAlaArgGlyLeu 119
301 TTTGGTTCTAGCCCAATTTGATTTTTCATGTGTTGGCGTCAAGCAACCC 350

seq_name: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:AAW90933

seq_documentation_block:

ID AAW90933 standard; Protein; 470 AA.

AC AAW90933;

DT 08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Neu 1 protein.

KW Fas; antibody; human; anti-inflammatory; anti-neuritic; antidiabetic;
KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thymometric; antihematic; anti-Fas;
KW nephrotropic; infertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic; lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; rheuma; Addison's disease; scleroderma; steatosis;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

05 Synthetic

PN EP990663-A2.

05-APR-2000

29-SEP-1999. 09EPB-0307711

30-SEP-1998: 08TR-0276981

PR 30-SEP-1998; 98JP-02/6882.

PA (SANY) SANKYO CO LTD.

PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

DR WPI; 2000-258930/23.

XX

PT	New humanized anti-Fas antibody, useful for treating or preventing e.g.,
PT	inflammatory or autoimmune disease, induces apoptosis selectively in
PT	cells with abnormal Fas-Fas ligand systems -

PS Claim 2; Page 169-170; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory
CC anti-neuritic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antineuritic, nephrotropic, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis fulminant, chronic, viral

(B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 1 which is described in the method of the invention.

SO Sequence 470 AA;

alignment_scores:

Quality: 500.50 Length: 125
Ratio: 4.469 Gaps: 2
Percent Similarity: 89.600 Percent Identity: 77.600

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAW90933 ..

Align seg 1/1 to: AAW90933 from: 1 to: 470

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1 CAATGCCAAGTGTGCAATCCGGCCCGAGGTCAGAGACCGAGGGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGlyValLysProGlyAlaSer 36
51 AGTCAAGTGTCTGCTAAGCTAGCGGCTATTTCTATTAATTTGA 100
|||||
36 TValLysValSerCysLysAlaSerGlyTyrThrPheThrSerTyrTPM 53
101 TTCAATGGGTGTCGACGCCCCCGGAGGGCTGGAATGATGGTGAG 150
|||||
53 etGlnTyrValLysGlnAlaProGlyGlnGlyLeuGlnTyrPheTgtGlu 69
151 ATCTTACCGGGCTCTGTAGACGCAATATACCGAAATTTTAAAGCCG 200
|||||
70 IleAspProSerAspSerTyrThrAsnTyrAsnGlnLysPheLysGly 86
201 TGTACTATGACGGCTGACACTGACATGATGATGATGATGACGCTCT 250
|||||
86 SalAlaThrLeuThrValAlaSerThrSerThrAlaTyrMetGluLeuS 103
251 CCAGCTTCGATCGAGGACACGCGCTATTTATTTGCGCGCT .. 294
|||||
103 etSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgAsnArg 119
295 ...TATTTTGTGTTCTAGCCGGAATTTGATTTTGGTGGGCTCA 341
|||||
120 AspTyr.....SerAsnAsnTyrPyrPheAspValTyrPylGly 132
342 AGGAACCTGTCGACTGTCGAGC 366
|||||
132 nGlyThrLeuValTyrValSerSer 140

```

seq_name: /SIDS8/gcgcdata/geneseq/geneseq/AA2000.DAT:AAW90934

seq_documentation_block:

ID AAW90934 standard; Protein: 470 AA.

AC AAW90934;
XX
XX
DT 08-AUG-2000 (first entry)
XX
XX

DE Humanised anti-Fas designed heavy chain Heu 2 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; antifertility; neuroprotective; arteriosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjoren's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture's syndrome; Crohn's disease; sterility; myasthenia gravis;

KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

PN EP990663-A2.

PD 05-APR-2000.

PE 29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

PA (SANY) SANKYO CO LTD.

PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

PI WPI; 2000-258930/23.

DR N-PSDB; AAA11645.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.

PT inflammatory or autoimmune disease, induces apoptosis selectively in

PT cells with abnormal Fas-Fas ligand systems

PS Claim 2 ; Page 174-176; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antifertility, neuroprotective, antiatherosclerotic, cardiac and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjoren's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention.

SO Sequence 470 AA;

alignment_scores:

Quality: 499.50 Length: 125
Ratio: 4.460 Gaps: 2
Percent Similarity: 89.600 Percent Identity: 77.600

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAW90934 ..

Align seg 1/1 to: AAW90934 from: 1 to: 470

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1 CAATGCCAAGTGTGCAATCCGGCCCGAGGTCAGAGACCGAGGGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGlyValLysProGlyAlaSer 36

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51 AGCAAGTCTCTCTGAAGCTAGCGCTATTTTCTAATTATGGA 100
   |||||
36 rVallysValSerCysAlaSerIleuThrPheThrSerTrpM 53
   |||||
101 TTCAATGGGTGCTCAGCCCCGGGAGGCGCTGAATGATGAGT 150
   |||||
53 eGlnIleuPallysGlnAlaProGlyGlnIleuGluTrpMetG 69
   |||||
151 ATCTACCGGGCTGTGTAGACACCGAATATACGAAATTTTAA 200
   |||||
70 IleAspProSerAspSerIleuThrAsnIleuGlnIleuS 86
   |||||
201 TGTTCATATGACCGCTGACACTGACATGATATGATGAGCT 250
   |||||
86 sAlaThrIleuThrValAspThrSerThrIleuAlaIleu 103
   |||||
251 CCAGCTCGCATCGAGACAGCGCGCTATATTGCGCGCT 294
   |||||
103 erSerIleuArgSerGlnAspThrAlaValIleuIleuIle 119
   |||||
295 ...TATTTTGGTTCTAGCCCGAATGATTTGATGTTGGGCT 341
   |||||
120 AspTyr.....SerAsnAsnTrpTyrPheAspValTrpG 132
   |||||
342 AGAACCCTGGTCACTGCTCCGAGC 366
   |||||
132 nGlyThrIleuValThrValSerSer 140

seq_name: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62210
seq_documentation_block:
ID   AAW62210 standard; Protein: 139 AA.
AC   AAW62210;
XX
DT   21-SEP-1998 (first entry)
DE   Humanised anti-HM1.24 antibody H chain V region HEF-RVHb-AHM g-gamma-1.
KW   Mouse; human; humanised; anti-HM1.24 antibody; myeloma; FR: CDR;
XX   framework region; complementarity determining region; antigenicity.
OS   Synthetic.
OS   Mus sp.
OS   Homo sapiens.
XX
PN   W09814580-A1.
XX
PD   09-APR-1998.
XX
PF   03-OCT-1997; 97WO-JP03553.
XX
PR   04-OCT-1996; 96JP-0264756.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Koishihara Y, Kosaka M, Ohtomo T, Ono K, Tsuchiya M;
XX   Yoshimura Y;
DR   WPI; 1998-286421/25.
XX   N-PSDB; AAV39399.
XX
PT   Humanised anti-HM1.24 antibody - for treatment of myeloma
PS   Example 9; Page 108-109; 210pp: Japanese.
XX
CC   A humanised anti-HM1.24 antibody has been developed which comprises
CC   human L and H chain C regions, and L and/or H chain V regions
CC   containing material originating in mouse anti-HM1.24 antibody. The V
CC   regions contain framework (FR) regions of human origin and
CC   complementarity determining regions (CDR) of mouse origin, leading to
CC   a reshaped humanised antibody. The C regions are human Ck (L-chain) and
CC   human C gamma (especially C gamma 1) (H-chain). The FR regions of the

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CC   L chain V region are derived from human subtype HSG1 (e.g. from human
CC   antibody RE1) and the FR regions of the H chain V region are derived
CC   from human subtype HSG1 (e.g. FR1-3 from human antibody Hg3 and FR4
CC   from human antibody J6). The present sequence represents an H chain
CC   V region from the present invention. The antibodies are used for
CC   the treatment of myeloma, especially by injection, intravenously,
CC   intramuscularly or subcutaneously. The antibodies are used at 0.01-1000
CC   (especially 5-100) mg/kg body weight. The humanised antibody has low
CC   antigenicity and is therefore effective therapeutically in humans.
XX
SQ   Sequence 139 AA;

alignment_scores:
  Quality: 499.00      Length: 122
  Ratio: 4.536        Gaps: 1
  Percent Similarity: 90.164      Percent Identity: 78.689

alignment_block:
  US-08-487-283a-12_COPY_58_423 x AAW62210 ..
  Align seg 1/1 to: AAW62210 from: 1 to: 139

1  CAAGTCCAACTGTGTCATCCGGGCGCGAGGTCAAGAACCGGCGCTC 50
   |||||
20  GlnValGlnIleuValGlnSerIleuAlaGlnValLysLysProGlyAla 36
   |||||
51  AGTCAAAAGTCTCTGTAAGCTAGCGGCTATTTTCTAATTATGGA 100
   |||||
36  rVallysValSerCysLysAlaSerGlyTyrThrPheThrProTyrTrpM 53
   |||||
101  TTCAATGGGTGCTGTCAGACCGCCCGGAGGCGCTGAATGATGAGCTG 150
   |||||
53  eGlnIleuPallysGlnAlaProGlyGlnIleuGluTrpMetGlySer 69
   |||||
151  ATCTACCGGGCTGTGTAGACACCGAATATACGAAATTTTAAAGCG 200
   |||||
70  IlePheProGlyAspGlyAspThrArgTyrSerGlnLysPheLysGly 86
   |||||
201  TGTTCATATGACCGCTGACACTGACATGATGATGATGAGCTCT 250
   |||||
86  sValThrMetThrAlaAspThrSerThrSerThrValIleuMetGlyLeu 103
   |||||
251  CCAGCTCGCATCGAGACAGCGCGCTATATTGCGCGCTTATTTT 300
   |||||
103  erSerIleuArgSerGlnAspThrAlaValIleuIleuIleuIleu 119
   |||||
301  TTGCTTCTAGCCGAATTTGATGATGTTGGGTCAGAGAACCT 350
   |||||
120  ....ArgArgGlyGlyTyrTyrPheAspTyrTrpGlyGlnIleu 134
   |||||
351  GGTCACTGTCGAGC 366
   |||||
134  rValThrValSerSer 139

seq_name: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02556
seq_documentation_block:
ID   AAV02556 standard; Protein: 139 AA.
AC   AAV02556;
XX
DT   16-JUL-1999 (first entry)
DE   Humanised H chain V region of antiHM1.24 antibody.
XX
CC   Reconstituted human antibody; peptide antigen HM1.24; framework region;
CC   complementary determining region; CDR: anti-HM1.24 antibody; myeloma;
CC   humanised antibody.
XX
OS   Synthetic.
OS   Mus sp.
XX

```



```

101 TTCATGGGCTGTCAGCCCGGGCAGGCGCTGGAATGATGGGTGAG 150
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
53 euglutrvalarglnalaprpglyhisglutrlprvalglylu 69
151 ATCTACCGGCTCTGTAGACCGAATATACCGAAATTTTAAGACCG 200
      ||| |||:::||||:||||:||||:||||:||||| 11
70 lleserproglythrphethrthrasntryasnglulysphelysalaar 86
201 TGTACTATGACGCGTGACACTTCGACTAGTACATATACATGAGCTCT 250
      ::::::::::| | | | | | | | | | | | | | | | | | | | | |
86 galatrhrphethrthralaasprlnserthrlnsrthralatrymetgluleus 103
251 CCAGCTGCGATCGAGGACACGCGCTCTATTTATTCGCGCGCTATTTT 300
      ||| | | | | | | | | | | | | | | | | | | | | | | | |
103 erseleuargsergluaspthrvalaValtyrtyrcysalalarpheser 119
301 TTTGGTTCATCCGAATTGG...TATTTGATGTTGGGCTCAGCAAGAAC 347
      ||::: ||::: ||| | | | | | | | | | | | | | | | | |
120 Hispheserglyserasntryasprtyrphesaprytyrtpglnglyth 136
348 CCGTGCACCTGCTCGAGC 366
      ||| | | | | | | | | | | | | | | | | | | | | | | | |
136 lleuvalthrvalser 142

seq_name: /cgn2.6/ptodata/2/1aa/6A_COMB.pep:US-08-127-721A-14

seq_documentation_block:
: Sequence 14, Application US/08127721A
: Patent No. 6066718
: GENERAL INFORMATION:
: APPLICANT: Hardman, No. 6066718man
: APPLICANT: Kolbinger, Frank
: APPLICANT: Saidanba, Jose
: TITLE OF INVENTION: Reshaped monoclonal antibodies against an
: TITLE OF INVENTION: Immunoglobulin isotype
: NUMBER OF SEQUENCES: 55
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6066718artis Patent and Trademark Department
: STREET: 59 Route 10
: CITY: East Hanover
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07936-1080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/127,721A
: FILING DATE: 27-SEPTEMBER-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/952,802
: FILING DATE: 25-SEPTEMBER-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 6066718ak, Henry P.
: REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 277-5110
: TELEFAX: (908) 277-4306
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 142 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-127,721A-14

alignment_scores:
Quality: 493.50 Length: 123

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Ratio: 4.446 Gaps: 1
Percent Similarity: 90.244 Percent Identity: 77.236

alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-127-721A-14 ..
Align seg 1/1 to: US-08-127-721A-14 from: 1 to: 142

1 CAAGTCCAACTGTGTCATTCGCGCGCGGAGTCAAGAAGCAGGCGCTTC 50
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20 GluValGlnleuValGlnserGlyAlaGluValLysIysproGlyAla 36
51 AGTCAAGATGTCCTGTAAAGCTAGCGGCTATATTTTTCATTAATTTGA 100
      ||| | | | | | | | | | | | | | | | | | | | | | | |
36 rValLysValserCysLysAlaSerGlyTrpThrPheserMetYrtrpL 53
101 TTCATAGGCTGCTCAGCGCCCGGCGAGGCGCTCGAATGATGCGTGAG 150
      ::::::::::| | | | | | | | | | | | | | | | | | | | | |
53 euglutrvalarglnalaprpglyhisglutrlprvalglylu 69
151 ATCTACCGGCTCTGTAGACCGAATATACCGAAATTTTAAGACCG 200
      ||| | | | | | | | | | | | | | | | | | | | | | | |
70 lleserproglythrphethrthrasntryasnglulysphelysalaar 86
201 TGTACTATGACGCGTGACACTTCGACTAGTACATATACATGAGCTCT 250
      ::::::::::| | | | | | | | | | | | | | | | | | | | | |
86 galatrhrphethrthralaasprlnserthrlnsrthralatrymetgluleus 103
251 CCAGCTGCGATCGAGGACACGCGCGCTCTATTTATTCGCGCGCTATTTT 300
      ||| | | | | | | | | | | | | | | | | | | | | | | |
103 erseleuargsergluaspthrvalaValtyrtyrcysalalarpheser 119
301 TTTGGTTCATCCGAATTGG...TATTTGATGTTGGGCTCAGCAAGAAC 347
      ||::: ||::: ||| | | | | | | | | | | | | | | | | |
120 Hispheserglyserasntryasprtyrphesaprytyrtpglnglyth 136
348 CCGTGCACCTGCTCGAGC 366
      ||| | | | | | | | | | | | | | | | | | | | | | | |
136 lleuvalthrvalser 142

seq_name: /cgn2.6/ptodata/2/1aa/6A_COMB.pep:US-08-485-246A-14

seq_documentation_block:
: Sequence 14, Application US/08485246A
: Patent No. 6072035
: GENERAL INFORMATION:
: APPLICANT: Hardman, No. 6072035man
: APPLICANT: Kolbinger, Frank
: APPLICANT: Saidanba, Jose
: TITLE OF INVENTION: Reshaped monoclonal antibodies against an
: TITLE OF INVENTION: Immunoglobulin isotype
: NUMBER OF SEQUENCES: 55
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6072035artis Patent Department
: STREET: 59 Route 10
: CITY: East Hanover
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07936-1080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,246A
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/127,721
: FILING DATE: 27-SEPTEMBER-1993
: APPLICATION NUMBER: US 07/952,802
: FILING DATE: 25-SEPTEMBER-1992

```

ATTORNEY/AGENT INFORMATION:
NAME: NO. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-246A-14

alignment_scores:
Quality: 493.50 Length: 123
Ratio: 4.446 Gaps: 1
Percent Similarity: 90.244 Percent Identity: 77.236

alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-485-246A-14 ..
Align seg 1/1 to: US-08-485-246A-14 from: 1 to: 142

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1 CAAGTCCAACTGGTGCATCCGCGCCGAGGTCAGAGCCAGGCGCTC 50
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51 AGTCAAGAGTCTCTTAAGCTAGCGGCTATATTTCATATTATGGA 100
|||||
36 rAllyValSerCysLysAlaSerGlyThrPheSerMetLysTrpL 53
101 TTCATGGGCGTGTGAGCCCGCGGAGGCGCTGGAATGATGGGAG 150
|||||
53 euGlnTrpValArgGlnAlaProGlyHisGlyLeuGlnTrpValG 69
151 ATCTTACCGGCGCTGTGAGCACCGCAATATACCAAAATTTTAAAG 200
|||||
70 IleSerProGlyThrPheThrThrAsnLysAsnGlnLysPheLys 86
201 TGTACTATGACGCGTGCACACTTGCAGTACATATACATGAGCTCT 250
|||||
86 gAlaThrPheThrAlaAspThrSerThrAsnThrAlaLysMetGlu 103
251 CCAGCTGCGATCGAGGACGCGCGCTCATATATGCGCGTATTTT 300
|||||
103 erSerLeuArgSerGlnAspThrAlaValLysTrpCysAlaArgPhe 119
301 TTTGGTCTAGCCCAATTGG...TATTTGATGTTGGGTCAGAGAAC 347
|||||
120 HisPheSerCylSerAsnTrpAspLysTrpPheAspLysTrpGln 136
348 CCTGCTCACTGCTCTGAGC 366
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136 rLeuValThrValSerSer 142
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seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-428-257A-78

seq_documentation_block:
Sequence 78, Application US/08428257A
Patent No. 5885808
GENERAL INFORMATION:
APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A.A.
TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-257A-78

alignment_scores:
Quality: 493.00 Length: 123
Ratio: 4.441 Gaps: 2
Percent Similarity: 90.244 Percent Identity: 78.862

alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-428-257A-78 ..
Align seg 1/1 to: US-08-428-257A-78 from: 1 to: 118

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1 CAAGTCCAACTGGTGCATCCGCGCCGAGGTCAGAGAACCCAGGCGCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAla 17
51 AGTCAAGAGTCTCTTAAGCTAGCGGCTATATTTCATATTATGGA 100
|||||
17 rAllyValSerCysLysAlaSerGlyThrPheSerAlaLysTrpL 34
101 TTCATGGGCGTGTGAGCCCGCGGAGGCGCTGGAATGATGGGAG 150
|||||
34 LeglutrValArgGlnAlaProGlyLysGlyLeuGlnTrpValGly 50
151 ATCTTACCGGCGCTGTGAGCACCGCAATATACCAAAATTTTAAAG 200
|||||
51 IleLeuProGlySerAsnAsnSerArgLysAsnGlnLysPheLysG 67
201 TGTACTATGACGCGTGCACACTTGCAGTACATATACATGAGCTCT 250
|||||
67 gValThrValThrArgAspThrSerThrAsnThrAlaLysMetGlu 84
251 CCAGCTGCGATCGAGGACGCGCGCTCATATATGCGCGCT...TAT 297
|||||
84 erSerLeuArgSerGlnAspThrAlaValLysTrpCysAlaArgSer 100
298 TTTTGGTCTAGCCCAATTGGTATTTGATGTTGGGTCAGAGAAC 347
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101 AspPheAla.....TrpPheAlaLysTrpGlnGlnGlyTh 112
348 CCTGCTCACTGCTCTGAGC 366
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112 rLeuValThrValSerSer 118
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seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-07-987-264-60

seq_documentation_block:
Sequence 60, Application US/07987264
Patent No. 6204366
GENERAL INFORMATION:
APPLICANT: VERHOEYEN, MARTINE ELISA
TITLE OF INVENTION: SPECIFIC BINDING AGENTS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

```

: STREET: 1100 NEW YORK AVENUE, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005-3918
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/987,264
: FILING DATE: 08-MAR-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9019553.8
: FILING DATE: 07-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB PCT/GB91/01511
: FILING DATE: 05-SEP-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: KOKULIS, PAUL N.
: REGISTRATION NUMBER: 16,773
: REFERENCE/DOCKET NUMBER: 200232/P30950USA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 861-3000
: TELEFAX: (202) 822-0944
: TELEX: 6714627 CUSH
: INFORMATION FOR SEQ ID NO: 60:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 118 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-987-264-60

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alignment_scores:
  Quality: 493.00      Length: 123
  Ratio: 4.441        Gaps: 2
  Percent Similarity: 90.244      Percent Identity: 78.862

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-07-987-264-60 ..

Align seg 1/1 to: US-07-987-264-60 from: 1 to: 118

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1 CAAGTCCAAGTGTGCAATCCGCGCGAGGTCAAGAGCCAGGGGCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaI 17
51 AGTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTTAATTATGGA 100
|||||
17 rValLysValSerCysLysAlaSerGlyTyrThrPheSerAlaTyrTrpI 34
101 TTCATGCGGTCGTACAGCCCGCGCGGCGCTGAAATGATGGGTGAG 150
|||||
34 leuIrrPValAlaGlnAlaProGlyLysGlyLeuGluTrpValGlyI 50
151 ATCTTACCGGGCTCTGTAGACCGCAATATACCAAAATTTTAAAGACCG 200
|||||
51 IleLeuProGlySerAsnAsnSerIrgYrAsnGluLysPheLysGlyY 67
201 TGTACTATGACGCGTGACACTTGACTAGTACATATACATGAGCTCT 250
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67 gValThrValAlaThrIrgAspTrnSerThrAsnThrAlaTyrMetGlu 84
251 CCACCTCGCGGTTCGAGACAGACGCGGCTATATATGCGCGGCT...TAT 297
|||||
84 erSerLeuAlaGSerGlnAspThrAlaValIYrTyrCysAlaIrgSerY 100
298 TTTTGTGGTCTACGCCGAATGTGATTTTGTATGTTTGGGGTCAAGAAC 347

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|||||
101 AspPheAla.....TrrPheAlaTyrTrpLysGlnGlyTh 112
348 CCGTGTCACTGTCTGAGC 366
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112 rLeuValThrValSerSer 118

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seq_name: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:US-08-476-176B-18

seq_documentation_block:

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: Sequence 18, Application US/08476176B
: Patent No. 5958708
: GENERAL INFORMATION:
: APPLICANT: Hardman, No. 5958708man
: APPLICANT: Kolbinger, Frank
: APPLICANT: Saldanha, Jose
: TITLE OF INVENTION: Reshaped monoclonal antibodies against an
: NUMBER OF SEQUENCES: 55.
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 5958708artis Patent Department
: STREET: 59 Route 10
: CITY: East Hanover
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07936-1080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/476,176B
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/127,721
: FILING DATE: 27-SEPTEMBER-1993
: APPLICATION NUMBER: US 07/952,802
: FILING DATE: 25-SEPTEMBER-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5958708ak, Henry P.
: REGISTRATION NUMBER: 33,200
: REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 277-5110
: TELEFAX: (908) 277-4306
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 142 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-476-176B-18

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alignment_scores:
  Quality: 492.50      Length: 123
  Ratio: 4.477        Gaps: 1
  Percent Similarity: 89.431      Percent Identity: 78.049

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-08-476-176B-18 ..

Align seg 1/1 to: US-08-476-176B-18 from: 1 to: 142

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20 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaI 36
51 AGTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTTAATTATGGA 100
|||||
36 rValLysValSerCysLysAlaSerGlyTyrTrnPheSerMetYrTrpL 53

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101 TTCAATGGGTGCGTACAGCCCGCCGAGGCGCTGGAATGATGGGTGAG 150
53 EUGLUTRPVALARGINALAPPTHRSERLASERTHRALATYRMETGLULEUS 69
151 ATCTACCGGCGCTGTGTAGACACGCAATATACGAAATTTTAAAGACCG 200
70 ILESERPROGLYTHRPHETHRTHRASNTYRASNGLULSPHELYSALAAR 86
201 TGTACTATGACGCGTGACACTTCGACTAGTACATGATACATGAGCTCT 250
86 GALATHRPHETHRALASPPTHRSERLASERTHRALATYRMETGLULEUS 103
251 CCAGCCTGCGATCGAGACGACGCGCGCTATATTATTCGCGCGCTATT 300
103 ERSERLEUARGSERGLUASPPTHRALAVALTYYTYRCYSALAARGPHESE 119
301 TTTGGTTGACCGCGAATTGG...TATTTGATNGTTGGGGGCAAGAAC 347
120 HISPHESERGLYSERASNTRYRASPTRYRPHASPTYYTRTPGLYINGLY 136
348 CCGTGCTACACTGTCTGAGC 366
136 RLEUVALTHRVALSER 142

seq_name: /cgn2_6/prodata/2/1aa/6A_COMB.pep:US-08-127-721A-18

seq_documentation_block:
; Sequence 18, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,721A
; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-127-721A-18

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Quality: 492.50      Length: 123
Ratio: 4.477
Percent Similarity: 89.431      Percent Identity: 78.049

Alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-127-721A-18
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20 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAla 36
51 AGTCAAACTGCTCTGTAAGCTAGCGGCTATATTTTCTAATATGGA 100
|||||
36 rValLysValSerGlyLysAlaSerGlyTYRThrPheSerMetTYRPL 53
101 TTCAATGGGTGCGTACAGCCCGCCGAGGCGCTGGAATGATGGGTGAG 150
|||||
53 EUGLUTRPVALARGINALAPPTHRSERLASERTHRALATYRMETGLUL 69
151 ATCTACCGGCGCTGTGTAGACACGCAATATACGAAATTTTAAAGACCG 200
|||||
70 ILESERPROGLYTHRPHETHRTHRASNTYRASNGLULSPHELYSALAAR 86
201 TGTACTATGACGCGTGACACTTCGACTAGTACATGATGAGCTCT 250
|||||
86 GALATHRPHETHRALASPPTHRSERLASERTHRALATYRMETGLULEUS 103
251 CCAGCCTGCGATCGAGACGACGCGCGCTATATTATTCGCGCGCTATT 300
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103 ERSERLEUARGSERGLUASPPTHRALAVALTYYTYRCYSALAARGPHESE 119
301 TTTGGTTGACCGCGAATTGG...TATTTGATNGTTGGGGGCAAGAAC 347
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120 HISPHESERGLYSERASNTRYRASPTRYRPHASPTYYTRTPGLYINGLY 136
348 CCGTGCTACACTGTCTGAGC 366
136 RLEUVALTHRVALSER 142

seq_name: /cgn2_6/prodata/2/1aa/6A_COMB.pep:US-08-485-246A-18

seq_documentation_block:
; Sequence 18, Application US/08485246A
; Patent No. 6072035
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6072035man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6072035artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,246A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802

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alignment_scores:


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; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: No. 6072035ak, Henry P.
;   REGISTRATION NUMBER: 33,200
;   REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (908) 277-5110
;   TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 18:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 142 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-246A-18

alignment_scores:
  Quality: 492.50      Length: 123
  Ratio: 4.477        Gaps: 1
  Percent Similarity: 89.431  Percent Identity: 78.049

alignment_block:
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20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
51 AGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATATTTGA 100
  ||||||||||||||||||||||||||||||||||||||||||||||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheSerMetLys 53
101 TTCATGGGTCGTCAGGCCCGCCGAGGCGCTGAATGATGGGTGAG 150
  ||||||||||||||||||||||||||||||||||||||||||||||||
53 euGluTyrValArgGlnAlaProGlyGlnArgLeuGluTyrMetGly 69
151 ATCTACCGGGCTCGTACGACGATATACCGAAATTTTAAAGACCG 200
  ||||||||||||||||||||||||||||||||||||||||||||||||
70 IleSerProGlyThrPheThrThrAsnTyrAsnGluLysPheLysAla 86
201 TGTACTATGACGCGTGACACTTCGACTAGTACATATACATGAGCTC 250
  ||||||||||||||||||||||||||||||||||||||||||||||||
86 gAlaThrPheThrAlaAspThrSerAlaSerThrLalaTyrMetGlu 103
251 CCAGCCCTGCGATCGAGAGACAGCGCGCTATATTTGCGCGCTATT 300
  ||||||||||||||||||||||||||||||||||||||||||||||||
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgPhe 319
301 TTTGGTCTACGCCGAATTGG..TATTTGATGTTGGGCGTCAAGAAC 347
  ||||||||||||||||||||||||||||||||||||||||||||||||
120 HisPheSerGlySerAsnTyrAspThrPheAspTyrTrpGlyGln 136
348 CCGTGCCTACTGCTCGAGC 366
  ||||||||||||||||||||||||||||||||||||||||||||||||
136 rLeuValThrValSerSer 142

seq_name: /cgn2.6/ptodata/2/iaa/5A_COMB pep:US-07-946-421-28
seq_documentation_block:
; Sequence 28, Application US/07946421
; Patent No. 5558864
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Kettleborough, Catherine A.
;   APPLICANT: Saidanha, Jose
;   TITLE OF INVENTION: Humanized and Chimeric Monoclonal
;   TITLE OF INVENTION: Antibodies
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Millen, White, Zelano & Branigan, P.C.

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; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/946,421
;   FILING DATE: 06-NOV-1992
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: WO PCT/EP92/00480
;     FILING DATE: 04-MAR-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: EP 911933892
;     FILING DATE: 06-MAR-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hamlet-King, Diana
;     REGISTRATION NUMBER: 33,302
;     REFERENCE/DOCKET NUMBER: Merck 1430
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 703-243-6333
;       TELEFAX: 703-243-6410
;       TELEX: 64191
;   INFORMATION FOR SEQ ID NO: 28:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 140 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
; US-07-946-421-28

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alignment_scores:
  Quality: 478.50      Length: 122
  Ratio: 4.350        Gaps: 1
  Percent Similarity: 90.164  Percent Identity: 76.230

alignment_block:
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20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
51 AGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATATTTGA 100
  ||||||||||||||||||||||||||||||||||||||||||||||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheSerSerHisTrp 53
51 ATCTTACCGGGCTCGTACGACCGCAATATACGAAATTTTAAAGACCG 200
  ||||||||||||||||||||||||||||||||||||||||||||||||
101 TTCATGGGTCGTCAGGCCCGCCGAGGCGCTGAATGATGGGTGAG 150
  ||||||||||||||||||||||||||||||||||||||||||||||||
53 ethIstrPvalArgGlnAlaProGlyGlnGlyLeuGluTyrPvalGly 69
151 ATCTTACCGGGCTCGTACGACCGCAATATACGAAATTTTAAAGACCG 200
  ||||||||||||||||||||||||||||||||||||||||||||||||
70 PheAsnProSerAsnGlyArgThrAsnTyrAsnGluLysPheLysSer 86
201 TGTACTATGACGCGTGACACTTCGACTAGTACATATACATGAGCTC 250
  ||||||||||||||||||||||||||||||||||||||||||||||||
86 gValThrMetThrLeuAspThrSerThrAsnThrAlaTyrMetGlu 103
251 CCAGCCCTGCGATCGAGAGACAGCGCGCTATATTTGCGCGCTATT 300
  ||||||||||||||||||||||||||||||||||||||||||||||||
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaSerArg 119
301 TTTGGTCTACGCCGAATTGGTATTTGATGTTGGGCGTCAAGACCT 350
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120 TyrAspTyrAspGlyArg...TyrPheAspTyrTrpGlyGlnGlyThr 135

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351 GGTCACTGCTGCAGC 366
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seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-09-199-149-12

seq_documentation_block:

; Sequence 12, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Truller, Stephen H.
; APPLICANT: Johnson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 12
; LENGTH: 128
; TYPE: PRT
; ORGANISM: murine B9
US-09-199-149-12

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Quality: 478.00 Length: 123
Ratio: 4.385 Gaps: 2
Percent Similarity: 88.618 Percent Identity: 77.236

alignment_block:

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Align seg 1/1 to: US-09-199-149-12 from: 1 to: 128

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51 AGTCAAGTCTGCTGTAAGCTAAGCGCTATATTTTCTAATTATGGA 100
|||||
22 rValLysValSerCysLysAlaSerGlyTyrThrPheSerSerTyrTrpI 39
101 TTCATAGGGTGGCTCAGAGCCCGGGCAGGGCCTGGAATGATGGGTGAG 150
|||||
39 leGluTrpValLysGlnAlaProGlyGlnIleuGluTrpIleGlyGlu 55
151 ATCTTACCGGGCTCTGTAGACACGAAATATACGAAATTTTAAAGCCG 200
|||||
56 lleuLeuProArgSerGlyAsnThrAsnTyrAsnGluLysPheLysGly 72
201 TGTACTATGACCGCTGACACTTGCAGCTAGTACATGATGAGGCTCT 250
|||||
72 salathrPheThrAlaAspThrSerThrAlaTyrMetGluLeuS 89
251 CCAGCTGCGATCGAGACACGCGCTATATATTC...GCGCGTTAT 297
|||||
89 erSerLeuArgSerGluAspThrAlaValTyrCysSerSerArgGly 105
298 TTTTGGTCTTACGCCGGAATTTGATTTGGGTTGGGCTCAAGAAC 347
|||||
106 valArgGlySer.....MetAspTyrTrpGlyGlnGlyTh 117
348 CCTGTCACCTGCTCGAGC 366
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117 rleuValThrValSerSer 123

seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-09-199-149-5

seq_documentation_block:

; Sequence 5, Application US/09199149

; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Truller, Stephen H.
; APPLICANT: Johnson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Humanized B9
US-09-199-149-5

alignment_scores:

Quality: 478.00 Length: 123
Ratio: 4.385 Gaps: 2
Percent Similarity: 88.618 Percent Identity: 77.236

alignment_block:

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Align seg 1/1 to: US-09-199-149-5 from: 1 to: 118

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51 AGTCAAGTCTGCTGTAAGCTAAGCGCTATATTTTCTAATTATGGA 100
|||||
17 rValLysValSerCysLysAlaSerGlyTyrThrPheSerSerTyrTrpI 34
101 TTCATAGGGTGGCTCAGAGCCCGGGCAGGGCCTGGAATGATGGGTGAG 150
|||||
34 leGluTrpValLysGlnAlaProGlyGlnIleuGluTrpIleGlyGlu 50
151 ATCTTACCGGGCTCTGTAGACACGAAATATACGAAATTTTAAAGCCG 200
|||||
51 lleuLeuProArgSerGlyAsnThrAsnTyrAsnGluLysPheLysGly 67
201 TGTACTATGACCGCTGACACTTGCAGCTAGTACATGATGAGGCTCT 250
|||||
67 salathrPheThrAlaAspThrSerThrAlaTyrMetGluLeuS 84
251 CCAGCTGCGATCGAGACACGCGCTATATATTC...GCGCGTTAT 297
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84 erSerLeuArgSerGluAspThrAlaValTyrCysSerSerArgGly 100
298 TTTTGGTCTTACGCCGGAATTTGATTTGGGTTGGGCTCAAGAAC 347
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101 valArgGlySer.....MetAspTyrTrpGlyGlnGlyTh 112
112 rleuValThrValSerSer 118
348 CCTGTCACCTGCTCGAGC 366
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seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-202-047-9

seq_documentation_block:

; Sequence 9, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.

```

? APPLICANT: BENDIG, Mary M.
? TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESS: Townsend and Townsend Hourie and Crew
? STREET: One Market Plaza, Steuart Tower, Suite 2000
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94105
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/202,047
? FILING DATE: 25-FEB-1994
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, William M.
? REGISTRATION NUMBER: 30,223
? REFERENCE/DOCKET NUMBER: 14137-77
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-326-2400
? TELEFAX: 415-326-2422
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 139 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-202-047-9

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alignment_scores:

Quality	473.00	Length:	124
Ratio:	4.339	Gaps:	2
Percent Similarity:	87.903	Percent Identity:	75.806

alignment_block:

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  |||||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrAsnTyrValM 53
  |||||||
101 TTCAATGGGTCGTGACGCCCGCGGCGGAGGGCTGAATGATGGGTGAG 150
  |||||||
53 ethLStrpValArgGlnAlaProGlyGlnArgLeuGluTrpMetGlyPhe 69
  |||||||
151 ATCTTACGGGCTCTGTAGCACCAGATATACCGAAATTTTAAAGACCG 200
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70 IleAsnProSerAsnAspGlyProLysTyrAsnGluArgPheLysAsnAr 86
  |||||||
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86 gValThrLleThrSerAspTrnSerAlaSerThrValaTyrMetGluLeuS 103
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345 AACCTGTGTCATGTCGACG 366
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? Sequence 9, Application US/08964690
? Patent No. 6033667
?
? GENERAL INFORMATION:
? APPLICANT: CHESNUT, Robert W.
? APPLICANT: POLLEY, Margaret J.
? APPLICANT: PAULSON, James C.
? APPLICANT: JONES, S. Tarian
? APPLICANT: SALDANHA, Jose W.
? APPLICANT: BENDIG, Mary M.
? TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESS: Townsend and Townsend Hourie and Crew
? STREET: One Market Plaza, Steuart Tower, Suite 2000
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94105
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/964,690
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/202,047
? FILING DATE: 25-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, William M.
? REGISTRATION NUMBER: 30,223
? REFERENCE/DOCKET NUMBER: 14137-77
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-326-2422
? TELEFAX: 415-326-2400
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 139 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-964-690-9

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alignment_scores:

Quality	473.00	Length:	124
Ratio:	4.339	Gaps:	2
Percent Similarity:	87.903	Percent Identity:	75.806

alignment_block:

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US-08-487-283A-12_COPY_58_423 x US-08-964-690-9 ..
Align seg 1/1 to: US-08-964-690-9 from: 1 to: 139

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51 AGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTCTATATTTGGA 100
  |||||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrAsnTyrValM 53
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101 TTCAATGGGTCGTGACGCCCGCGGCGGAGGGCTGAATGATGGGTGAG 150
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201 TGTATCTATGACGCGTGTACGACTGTACATGATATACATGAGACTCT 250
86 gValThrIleThrSerAspThrSerAlaSerThrAlaTyrMeGluLeuS 103
251 CCAGCCTGGGATCGAGACGACGCGCGTCTATATTTCGCGCGCTTATT 300
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArg..... 117
301 TTGGTTCACGCCG.....AATTGCTATTTTTGTATGTTGGGCTCAAG 344
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345 AACCGTGGTCACTGTCTCGAGC 366
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; Sequence 3, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trull Jr., Stephen H.
; APPLICANT: Johanson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Kabat VH subgroup I
; US-09-199-149-3

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alignment_scores:

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Quality: 472.50      Length: 126
Ratio: 4.375         Gaps: 2
Percent Similarity: 85.714      Percent Identity: 76.190

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alignment_block:

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Align seg 1/1 to: US-09-199-149-3 from: 1 to: 125

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1 |||||
1 rValLysValSerCysLysAlaSerGlyTyrThrPheThrSerTyrAla 34
101 TTCATGGTGTGTGTCAGCGCGCGCGAGGCGCTGGAATGAGAGGCGAG 150
1 |||||
34 leSerTrpAlaArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTrp 50
151 ATCTTACCGCGGCTGTGTAGCACCGCAATATACGAAATTTTAAAGCCG 200
1 |||||
51 IleasnProGly...GlyAspThrAsnTyrAlaGlnLysPheGlnGlyAr 66
201 TGTATCTATGACGCGTGTACGACTGTACATGATATACATGAGACTCT 250
1 |||||

```

```

66 gValThrIleThrAlaAspThrSerThrSerThrAlaTyrMeGluLeuS 83
251 CCAGCCTGGGATCGAGACGACGCGCGTCTATATTATGCGCGCT..... 294
83 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgProGly 99
295 .....TATTTTGTGTTCAGCCCGCAATGCTATTTTGTATGTTGGG 338
100 TyrGlyTyrGlyGlyGlyCysTyrGlyTyrTrpTyrTrpGlyValTrpG 116
116 yGlnGlyThrLeuValThrValSerSer 125

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seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-476-176B-12

seq_documentation_block:

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; Sequence 12, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-176B-12

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alignment_scores:

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Quality: 476.50      Length: 123
Ratio: 4.372         Gaps: 1
Percent Similarity: 88.618      Percent Identity: 73.984

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-08-476-176B-12 ..

Align seg 1/1 to: US-08-476-176B-12 from: 1 to: 142

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1 CAAGTCCAACTGTGTCATCCGGCCGAGGTCAAGAAGCCAGGGCCCTC 50
   |||||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysLysProGlyAlaSe 36
   |||||
51 AGTCAAGTGTCCCTGAAGCTAGCGGCTATATTTTCTAATTAATTGA 100
   |||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheSerMetYrTrpL 53
   |||||
101 TTCATGGGTGCTCAGGCCCGGGCAGGGCTCGAATGGATGGGTGAG 150
   :::::
53 euGlnTrpValLysGlnArgProGlyHisGlyLeuGlnTrpValGlyGlu 69
   |||||
151 ATCTTACCGGGCTCTGTAGCACCGCAATATACGAAATTTTAAAGACCG 200
   ||| |||||
70 IleSerProGlyThrPheThrThrAsnTyrAsnGlnLysPheLysAlaLys 86
   :::::
201 TGTACTATGACGGCTGACACTTGCAGTACAGTATACATGAGCTCT 250
   :::::
86 sAlaThrPheThrAlaAspThrSerThrAsnThrAlaTyrMetGlnLeus 103
   :::::
251 CCAAGCTGCGATCGGAGACACAGGGCGCTATATTATTCGGCGGTATT 300
   |||||
103 erSerLeuThrSerGlnAspThrAlaValTyrCysAlaArgPheSer 119
   |||||
301 TTTGGTTCTAGCCCGAATTGG...TATTTGATGTTTGGGGTCAAGAAG 347
   |||||
120 HisPheSerGlySerAsnTyrAspTyrPheAspTyrTrpGlyGlnGlyTh 136
   |||||
348 CCTGGTCACTGTCTCGAGC 366
   |||||
136 rLeuValThrValSerSer 142
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Items Description

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HIGHLIGHT set on as ''

HIGHLIGHT set on as ''

? begin 5,73,155,399,357

10nov00 09:22:02 User208760 Session D1713.2

\$0.00 0.055 DialUnits File410

\$0.00 Estimated cost File410

\$0.01 TYMNET

\$0.01 Estimated cost this search

\$0.46 Estimated total session cost 0.169 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 5:Biosis Previews(R) 1969-2000/Nov W2

(c) 2000 BIOSIS

File 73:EMBASE 1974-2000/Oct W3

(c) 2000 Elsevier Science B.V.

*File 73: Update codes are currently undergoing readjustment.

For details type Help News73.

File 155:MEDLINE(R) 1966-2000/Dec W4

(c) format only 2000 Dialog Corporation

*File 155: For changes to the file and check tags information
please see Help News155.

File 399:CA SEARCH(R) 1967-2000/UD=13320

(c) 2000 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement.

RANK charge added; see HELP RATES 399.

File 357:Derwent Biotechnology Abs 1982-2000/Nov B2

(c) 2000 Derwent Publ Ltd

Set Items Description

? s 5g1? and (c5 or c5a or complement)

89 5G1?

19902 C5

8617 C5A

237256 COMPLEMENT

S1 6 5G1? AND (C5 OR C5A OR COMPLEMENT)

? rd s1

...completed examining records

S2 2 RD S1 (unique items)

? t s2/3/all

2/3/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2000 BIOSIS. All rts. reserv.

10974348 BIOSIS NO.: 199799595493

Inhibition of **complement** activity by humanized anti-C5 antibody
and single-chain Fv.

AUTHOR: Thomas Thomas C(a); Rollins Scott A; Rother Russell P; Giannoni
Michelle A; Hartman Sandra L; Elliott Eileen A; Nye Steven H; Matis Louis
A; Squinto Stephen P; Evans Mark J

AUTHOR ADDRESS: (a)Alexion Pharmaceuticals, 25 Science Park, New Haven, CT
06511**USA

JOURNAL: Molecular Immunology 33 (17-18):p1389-1401 1996 (1997)
ISSN: 0161-5890
RECORD TYPE: Abstract
LANGUAGE: English

2/3/2 (Item 1 from file: 357)
DIALOG(R) File 357:Derwent Biotechnology Abs
(c) 2000 Derwent Publ Ltd. All rts. reserv.

0190050 DBA Accession No.: 96-00821 PATENT
Treating glomerulonephritis with antibody against **complement-C5**
component - antiinflammatory monoclonal antibody production from
hybridoma cell culture, and Fv single chain antibody engineering
AUTHOR: Evans M J; Matis L; Mueller E E; Nye S H; Rollins S; Rother R
P; Springhorn J P; Squinto S P; Thomas T C; Wang Y; Wilkins J A
CORPORATE SOURCE: New Haven, CT, USA.
PATENT ASSIGNEE: Alexion-Pharm. 1995
PATENT NUMBER: WO 9529697 PATENT DATE: 951109 WPI ACCESSION NO.:
95-392923 (9550)
PRIORITY APPLIC. NO.: US 236208 APPLIC. DATE: 940502
NATIONAL APPLIC. NO.: WO 95US5688 APPLIC. DATE: 950501
LANGUAGE: English
? s (c5)(20n)(c5a)(20n)(antibod?)

>>>Operator "(5C)" in invalid position
? s (antibod?)(20n)(c5)(20n)(c5a)

>>>Operator "(5C)" in invalid position
? ds

Set	Items	Description
S1	6	5G1? AND (C5 OR C5A OR COMPLEMENT)
S2	2	RD S1 (unique items)
? s antibod?(10n)(c5 or c5a or complement)		
	1604233	ANTIBOD?
	19902	C5
	8617	C5A
	237256	COMPLEMENT
S3	52782	ANTIBOD?(10N)(C5 OR C5A OR COMPLEMENT)
? s antibod?(10n) c5 (10n) c5a		
	1604233	ANTIBOD?
	19902	C5
	8617	C5A
S4	106	ANTIBOD?(10N) C5 (10N) C5A
? rd s4		

...examined 50 records (50)
...examined 50 records (100)
...completed examining records
S5 52 RD S4 (unique items)
? t s5/7/all

s (c5) (20n) (c5a) (20n) (antibod?)

>>>Operator "(5C)" in invalid position
? s (antibod?) (20n) (c5) (20n) (c5a)

>>>Operator "(5C)" in invalid position
? ds

Set	Items	Description
S1	6	5G1? AND (C5 OR C5A OR COMPLEMENT)
S2	2	RD S1 (unique items)

? s antibod?(10n) (c5 or c5a or complement)

	1604233	ANTIBOD?
	19902	C5
	8617	C5A
	237256	COMPLEMENT
S3	52782	ANTIBOD?(10N) (C5 OR C5A OR COMPLEMENT)

? s antibod?(10n) c5 (10n) c5a

	1604233	ANTIBOD?
	19902	C5
	8617	C5A
S4	106	ANTIBOD?(10N) C5 (10N) C5A

? rd s4

...examined 50 records (50)
...examined 50 records (100)
...completed examining records
S5 52 RD S4 (unique items)
? t s5/7/all

File 73:EMBASE 1974-2000/Oct W3
 (c) 2000 Elsevier Science B.V.
 *File 73: Update codes are currently undergoing readjustment.
 For details type Help News73.
 File 155:MEDLINE(R) 1966-2000/Dec W4
 (c) format only 2000 Dialog Corporation
 *File 155: For changes to the file and check tags information
 please see Help News155.
 File 399:CA SEARCH(R) 1967-2000/UD=13320
 (c) 2000 American Chemical Society
 *File 399: Use is subject to the terms of your user/customer agreement.
 RANK charge added; see HELP RATES 399.
 File 357:Derwent Biotechnology Abs 1982-2000/Nov B2
 (c) 2000 Derwent Publ Ltd

Set	Items	Description
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? b 410		
>>>'IALOG' not recognized as set or accession number		
? set hi ;set hi		

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10nov00 09:55:25 User208760 Session D1713.4
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$0.13 Estimated cost File5
$0.20      0.024 DialUnits File73
$0.20 Estimated cost File73
$0.08      0.024 DialUnits File155
$0.08 Estimated cost File155
$0.30      0.024 DialUnits File399
$0.30 Estimated cost File399
$0.28      0.024 DialUnits File357
$0.28 Estimated cost File357
OneSearch, 5 files, 0.119 DialUnits FileOS
$0.05 TYMNET
$1.04 Estimated cost this search
$1.04 Estimated total session cost 0.119 DialUnits
  
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File 410:Chronolog(R) 1981-2000 Sep/Oct
 (c) 2000 The Dialog Corporation plc

Set	Items	Description
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HILIGHT set on as ''		
HILIGHT set on as ''		
? begin 5,73,155,399,357		

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10nov00 09:55:45 User208760 Session D1713.5
$0.00      0.059 DialUnits File410
$0.00 Estimated cost File410
$0.02 TYMNET
$0.02 Estimated cost this search
$1.06 Estimated total session cost 0.178 DialUnits
  
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SYSTEM:OS - DIALOG OneSearch
 File 5:Biosis Previews(R) 1969-2000/Nov W2
 (c) 2000 BIOSIS
 File 73:EMBASE 1974-2000/Oct W3

(c) 2000 Elsevier Science B.V.
 *File 73: Update codes are currently undergoing readjustment.
 For details type Help News73.
 File 155:MEDLINE(R) 1966-2000/Dec W4
 (c) format only 2000 Dialog Corporation
 *File 155: For changes to the file and check tags information
 please see Help News155.
 File 399:CA SEARCH(R) 1967-2000/UD=13320
 (c) 2000 American Chemical Society
 *File 399: Use is subject to the terms of your user/customer agreement.
 RANK charge added; see HELP RATES 399.
 File 357:Derwent Biotechnology Abs 1982-2000/Nov B2
 (c) 2000 Derwent Publ Ltd

Set	Items	Description
---	-----	-----
? s c5	(10n)	(alpha(w)chain) (10n) antibod?
	19902	C5
	1597067	ALPHA
	867947	CHAIN
	1604233	ANTIBOD?
S1	4	C5 (10N) (ALPHA(W)CHAIN) (10N) ANTIBOD?
? rd	s1	
...completed examining records		
	S2	2 RD S1 (unique items)
? t	s/7/all	
>>>Item list not allowed with accession number		
? t	s2/7/all	

2/7/1 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
 (c) 2000 BIOSIS. All rts. reserv.

08377954 BIOSIS NO.: 000094108458
 FORMATION AND STRUCTURE OF THE C5B-7 COMPLEX OF THE LYTIC PATHWAY OF
 COMPLEMENT
 AUTHOR: DISCIPIO R G
 AUTHOR ADDRESS: DEP. IMMUNOLOGY IMM18, RESEARCH INSTITUTE SCRIPPS CLINIC,
 10666 N. TORREY PINES RD., LA JOLLA, CALIF. 92037.
 JOURNAL: J BIOL CHEM 267 (24). 1992. 17087-17094.
 FULL JOURNAL NAME: Journal of Biological Chemistry
 CODEN: JBCHA
 RECORD TYPE: Abstract
 LANGUAGE: ENGLISH

ABSTRACT: The formation and structure of the complement cytolytic intermediary complex, C5b-7, were studied with the aim of determining the interactive regions of C5, C6, and C7. The structure of human complement component C5 was elucidated by the application of limited proteolysis which generated well characterized major polypeptide fragments of this molecule. Plasmin, thrombin, and kallikrein cleave C5b with greater facility than C5. The most useful cleavage of C5b was effected by plasmin because the fragmentation pattern was similar to the processing the C3b by factors H, I, and kallikrein. Plasmin hydrolyzes peptide bonds within the .alpha.'-chain of C5b, resulting in a four-chain fragment, C5c (Mr = 142,000), and a single chain fragment, C5d (Mr = 43,000). Circular dichroism spectroscopic analyses indicated that C5d is substantially richer in .alpha.-helical content than is C5c (27 versus 9%). Polyclonal **antibodies** directed against C5c blocked the interaction of C5b-6 with C7, whereas **antibodies** directed against C5d inhibited the binding of C5 with C3b. Chemical cross-linking using a cleavable radioiodinated photoreactive reagent revealed that both C6 and C7

associate preferentially with the .alpha.'-chain of C5b. The reversible interactions of C5 with C6, C7, and major polypeptide fragments derived from these were investigated with solid phase binding assays. The results indicate that the carboxyl-terminal domains of C6 and C7, which have cysteine-rich modules homologous to those found in factors H and I, have the capacity to link specifically with C5.

2/7/2 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
(c) 2000 Derwent Publ Ltd. All rts. reserv.

0190050 DBA Accession No.: 96-00821 PATENT
Treating glomerulonephritis with antibody against complement-C5 component
- antiinflammatory monoclonal antibody production from hybridoma cell
culture, and Fv single chain antibody engineering
AUTHOR: Evans M J; Matis L; Mueller E E; Nye S H; Rollins S; Rother R
P; Springhorn J P; Squinto S P; Thomas T C; Wang Y; Wilkins J A
CORPORATE SOURCE: New Haven, CT, USA.
PATENT ASSIGNEE: Alexion-Pharm. 1995
PATENT NUMBER: WO 9529697 PATENT DATE: 951109 WPI ACCESSION NO.:
95-392923 (9550)
PRIORITY APPLIC. NO.: US 236208 APPLIC. DATE: 940502
NATIONAL APPLIC. NO.: WO 95US5688 APPLIC. DATE: 950501
LANGUAGE: English
ABSTRACT: A new method for therapy of glomerulonephritis involves
introduction of an antibody (Ab) that binds to complement-C5 into the
bloodstream, to reduce the cell-lysing ability of complement present in
the blood. The Ab reduces conversion of complement-C5 to complement-C5a
and -C5b. The Ab may bind to C5b, and does not inhibit formation of
complement-C3b. The Ab may inhibit binding of C5 to complement-C3 or
complement-C4, by binding with a 5G46k, 5G27k, 5G325aa, 5G200aa or
KSSKC peptide fragment. A complete blockade of complement hemolytic
activity may occur. A monoclonal Ab (MAb) against human complement-
C5 **alpha-chain** or a peptide fragment, produced by
hybridoma 5G1.1 (ATCC HB 11625) is new. DNA encoding an Fv single chain
antibody with specified variable region light chain and heavy
chain sequences (including complementarity determining region-1, -2 and
-3) and an optional human constant domain is claimed, and may be
inserted in a vector for expression in a recombinant host cell. The MAb
eliminates glomerular inflammation and enlargement, and may also be
used in therapy of inflammatory joint disease or immunological or blood
disorders. (181pp)
? begin 652,653,654

10nov00 09:57:51 User208760 Session D1713.6
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\$1.65 1 Type(s) in Format 7
\$1.65 1 Types
\$2.77 Estimated cost File5
\$1.76 0.207 DialUnits File73
\$1.76 Estimated cost File73
\$0.66 0.205 DialUnits File155
\$0.66 Estimated cost File155
\$2.75 0.219 DialUnits File399
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\$0.63 0.053 DialUnits File357
\$2.20 1 Type(s) in Format 7
\$2.20 1 Types
\$2.83 Estimated cost File357
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\$0.15 TYMNET
\$10.92 Estimated cost this search
\$11.98 Estimated total session cost 1.061 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 652:US Patents Fulltext 1971-1979

(c) format only 2000 The Dialog Corp.

*File 652: Reassignment data current through 7/25/2000 recordings.
Due to recent processing problems, the SORT command is not working.

File 653:US Patents Fulltext 1980-1989

(c) format only 2000 The Dialog Corp.

*File 653: Reassignment data current through 7/25/2000 recordings.
Due to recent processing problems, the SORT command is not working.

File 654:US Pat.Full. 1990-2000/Nov 07

(c) format only 2000 The Dialog Corp.

*File 654: Reassignment data current through 7/25/2000 recordings.
Due to recent processing problems, the SORT command is not working.

Set Items Description

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? s c5 (10n) (alpha(w)chain) (10n) antibod?

19913 C5

310045 ALPHA

351863 CHAIN

45267 ANTIBOD?

S1 0 C5 (10N) (ALPHA(W)CHAIN) (10N) ANTIBOD?

5/7/52 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
(c) 2000 Derwent Publ Ltd. All rts. reserv.

0117029 DBA Accession No.: 91-04671 PATENT
Sensitive assay of complement-C5a peptide or des-Arg derivative - new
monoclonal antibody, anti-idiotypic monoclonal antibody and hybridoma
PATENT ASSIGNEE: Goetze O 1991
PATENT NUMBER: EP 411306 PATENT DATE: 910206 WPI ACCESSION NO.: 91-038259
(9106)

PRIORITY APPLIC. NO.: DE 3924924 APPLIC. DATE: 890727

NATIONAL APPLIC. NO.: EP 90111920 APPLIC. DATE: 900622

LANGUAGE: German

ABSTRACT: A method for the detection and/or quantitative determination of the complement peptides C5a and/or C5a-des-Arg (C5a') in biological fluid comprises immobilized antibodies (Ab 1) which bind C5a and C5a', and second detectable antibodies (Ab 2) which bind to C5a and/or C5a' bound to the first **antibodies**. The following are claimed: (1) cell lines producing monoclonal **antibodies** (MAbs) which bind to the receptor-binding sites in C5a and C5a' but not with the corresponding amino acid sequence in native C5; (2) MAbs produced by these cell lines; (3) anti-idiotypic (AIAb) against MAb produced by the specified cell lines; and (4) the cell line CNCM I-188 which produces AIAb F23/14. Ab 1 and Ab 2 are MAbs produced in mice or humans, and are MAb C17/5 (produced by the cell line CNCM I-887) and MAb G25/2 (produced by the cell line CNCM I-889), respectively. Compositions containing the MAbs can be used to treat and prevent diseases associated with elevated C5a levels in the blood or other disorders related to intra- or extra-vascular complement activation. AIAb can be used to block reaction of C5a with its receptors. (27pp)

03412845 EMBASE No: 1987165422

Rapid and simple measurement of human C5a-des-Arg level in plasma or serum using monoclonal antibodies

Takeda J.; Kinoshita T.; Takata Y.; et al.

Department of Bacteriology, Osaka University Medical School, Suita, Osaka 565 Japan

Journal of Immunological Methods (J. IMMUNOL. METHODS) (Netherlands) 1987, 101/2 (265-270)

CODEN: JIMMB

DOCUMENT TYPE: Journal

LANGUAGE: ENGLISH

A new sandwich immunoassay method for measuring human C5a-des-Arg was developed using monoclonal antibody specifically reactive with C5a-des-Arg. Monoclonal antibodies were obtained from a panel of hybridomas produced by fusion of mouse myeloma cells, P3 x 63-AG8,653, with spleen cells from a CBF1(C57BL/6 x BALB/c) mouse immunized with purified C5a. The reactivities of these monoclonal **antibodies** against C5a, C5a-des-Arg and C5 were tested by solid-phase radioimmunoassay. One of the **antibodies** reacted with C5a-des-Arg, but not with C5a and C5. By use of this **antibody** for capturing **antibody** in sandwich immunoassay, a rapid and simple method was developed for measuring C5a-des-Arg without previous removal of C5. The sensitivity of this assay system was approximately 1 ng/ml

5/7/35 (Item 4 from file: 73)
DIALOG(R)File 73:EMBASE
(c) 2000 Elsevier Science B.V. All rts. reserv.

07290420 EMBASE No: 1998173819
Immunotherapy for autoimmune and inflammatory renal diseases
Jayne D.R.W.
D.R.W. Jayne, Division of Renal Medicine, St George's Hospital Medical
School, London SW17 0RE United Kingdom
AUTHOR EMAIL: djayne@sghms.ac.uk
Current Opinion in Nephrology and Hypertension (CURR. OPIN. NEPHROL.
HYPERTENS.) (United Kingdom) 1998, 7/3 (311-315)
CODEN: CNHYE ISSN: 1062-4821
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 46

New treatments for autoimmune renal disease are required, and a developing knowledge of its underlying immunopathogenesis has identified sites where immunotherapy is likely to be effective. Experience with intravenous immunoglobulin and lymphocyte depletion by monoclonal antibodies in systemic vasculitis and systemic lupus erythematosus is awaiting confirmation by randomized trials. Treatments at or near clinical testing include monoclonal antibody blockade of leucocyte-endothelial interactions and CD40 mediated B-cell activation, and immunoablation with autologous stem- cell transplantation for more severe multisystem autoimmune disease.

06268778 BIOSIS NO.: 000086102961

DETECTION OF NATIVE HUMAN COMPLEMENT COMPONENTS C3 AND C5 AND THEIR
PRIMARY ACTIVATION PEPTIDES C3a AND C5a ANAPHYLATOXIC PEPTIDES BY
ELISA WITH MONOCLONAL ANTIBODIES

AUTHOR: KLOS A; IHRIG V; MESSNER M; GRABBE J; BITTER-SUERMAN D

AUTHOR ADDRESS: INST. MED. MICROBIOLOGY, HOCHHAUS AM AUGUSTUSPLATZ, 6500
MAINZ, WEST GERMANY.

JOURNAL: J IMMUNOL METHODS 111 (2). 1988. 241-252.

FULL JOURNAL NAME: Journal of Immunological Methods

CODEN: JIMMB

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Monoclonal antibodies (mAbs) were raised against human C3a, C3b, C5a, and C5b after immunization of BALB/c mice with the native components C3 and C5. Using different combinations of these mAbs we have developed four sensitive sandwich-enzyme-linked immunosorbent assays (ELISAs) for the detection of native C3 or C5 in samples with low concentrations of these proteins, e.g., in cell culture supernatants or synovial fluids and cerebrospinal fluids (CSF) and for the detection of the anaphylatoxic peptides (AT-peptides) C3a or C5a in human EDTA-plasma. The C3- and C5-ELISAs were found to be specific for the uncleaved complement proteins. Two different anti-C3a or anti-C5a mAbs were combined for the C3a- and C5a-eLISA. Before assaying a sample in the C3a- or C5a-ELISA a precipitation step to eliminate uncleaved C3 and C5 was necessary. The sensitivity and specificity of the four ELISAs were treated with purified antigens and EDTA-plasma or Cobra venom factor-activated EGTA-plasma samples as a source of C3a and C5a. The detection limits were 1 ng/ml for C3, 1 ng/ml for C3a, 2 ng/ml for C5, and 100 pg/ml for C5a. Plasma samples from patients undergoing cardiopulmonary bypass (CPB) surgery were used as a source of pathological material.

10225205 BIOSIS NO.: 199698680123

In vitro and in vivo inhibition of complement activity by a single-chain Fv fragment recognizing human C5.

AUTHOR: Evans Mark J(a); Rollins Scott A; Wolff Dennis W; Rother Russell P; Norin Allen J; Therrien Denise M; Grijalva Galo A; Mueller John P; Nye Steven H; Squinto Stephen P; Wilkins James A

AUTHOR ADDRESS: (a)Dep. Molecular Dev., Alexion Pharmaceuticals, 25 Science Park, New Haven, CT 06511**USA

JOURNAL: Molecular Immunology 32 (16):p1183-1195 1995

ISSN: 0161-5890

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Complement activation has been implicated in the pathogenesis of several human diseases. Recently, a monoclonal **antibody** (N19-8) that recognizes the human complement protein C5 has been shown to effectively block the cleavage of C5 into C5a and C5b, thereby blocking terminal complement activation. In this study, a recombinant N19-8 scFv **antibody** fragment was constructed from the N19-8 variable regions, and produced in both mammalian and bacterial cells. The N19-8 scFv bound human C5 and was as potent as the N19-8 monoclonal antibody at inhibiting human C5b-9-mediated hemolysis of chicken erythrocytes. In contrast, the N19-8 scFv only partially retained the ability of the N19-8 monoclonal antibody to inhibit C5a generation. To investigate the ability of the N19-8 scFv to inhibit complement-mediated tissue damage, complement-dependent myocardial injury was induced in isolated mouse hearts by perfusion with Krebs-Henseleit buffer containing 6% human plasma. The perfused hearts sustained extensive deposition of human C3 and C5b-9, resulting in increased coronary artery perfusion pressure, end-diastolic pressure, and a decrease in heart rate until the hearts ceased beating approximately 10 min after the addition of plasma. Hearts treated with human plasma supplemented with either the N19-8 monoclonal antibody or the N19-8 scFv did not show any detectable changes in cardiac performance for at least 1 hr following the addition of plasma. Hearts treated with human plasma alone showed extensive deposition of C3 and C5b-9, while hearts treated with human plasma containing the N19-8 scFv showed extensive deposition of C3, but no detectable deposition of C5b-9. Administration of a 100 mg bolus dose of N19-8 scFv to rhesus monkeys inhibited the serum hemolytic activity by at least 50% for up to 2 hr. Pharmacokinetic analysis of N19-8 scFv serum levels suggested a two-compartment model with a T-1/2-alpha of 27 min. Together, these data suggest the recombinant N19-8 scFv is a potent inhibitor of the terminal complement cascade and may have potential in vivo applications where short duration inhibition of terminal complement activity is desirable.

5/7/13 (Item 13 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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10061787 BIOSIS NO.: 199598516705

Anti-C5 monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease.

AUTHOR: Wang Yi(a); Rollins Scott A(a); Madri Joseph A; Matis Louis A(a)

AUTHOR ADDRESS: (a)Immunobiol. Program, Alexion Pharm. Inc., New Haven, CT 06511**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United

ABSTRACT: Activated components of the complement system are potent mediators of inflammation that may play an important role in numerous disease states. For example, they have been implicated in the pathogenesis of inflammatory joint diseases including rheumatoid arthritis (RA). To target complement activation in immune-mediated joint inflammation, we have utilized monoclonal **antibodies** (mAbs) that inhibit the complement cascade at C5, blocking the generation of the major chemotactic and proinflammatory factors C5a and C5b-9. In this study, we demonstrate the efficacy of a mAb specific for murine C5 in the treatment of collagen-induced arthritis, an animal model for RA. We show that systemic administration of the anti-C5 mAb effectively inhibits terminal complement activation in vivo and prevents the onset of arthritis in immunized animals. Most important, anti-C5 mAb treatment is also highly effective in ameliorating established disease. These results demonstrate a critical role for activated terminal complement components not only in the induction but also in the progression of collagen-induced arthritis and suggest that C5 may be an attractive therapeutic target in RA.

5/7/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

5/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10514607 BIOSIS NO.: 199699135752

Amelioration of lupus-like autoimmune disease in NZB/W F-1 mice after treatment with a blocking monoclonal antibody specific for complement component C5.

AUTHOR: Wang Yi(a); Hu Qile; Madri Joseph A; Rollins Scott A; Chodera Amy; Matis Louis A

AUTHOR ADDRESS: (a)Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT 06511**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 93 (16):p8563-8568 1996

ISSN: 0027-8424

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: New Zealand black times New Zealand white (NZB/W) F-1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus. Female NZB/W F-1 mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 months of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic complement activation, the role of proinflammatory complement components in disease progression has not been established. In this study we have examined the contribution of activated terminal complement proteins to the pathogenesis of the lupus-like autoimmune disease. Female NZB/W F-1 mice were treated with a monoclonal **antibody** (mAb) specific for the C5 component of complement that blocks the cleavage of C5 and thus prevents the generation of the potent proinflammatory factors C5a and C5b-9. Continuous therapy with anti-C5 mAb for 6 months resulted in significant amelioration of the course of glomerulonephritis and in markedly increased survival. These findings demonstrate an important role for the terminal complement cascade in the progression of renal disease in NZB//W F-1 mice, and suggest that mAb-mediated C5 inhibition may be a useful approach to the therapy of immune-complex glomerulonephritis in humans.

5/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10419584 BIOSIS NO.: 199699040729

Proteolytic inactivation of the leukocyte C5a receptor by proteinases derived from Porphyromonas gingivalis.

AUTHOR: Jagels Mark A(a); Travis James; Potempa Jan; Pike Robert; Hugli Tony E

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5/7/4 (Item 4 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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11517221 BIOSIS NO.: 199800298553

Myocardial infarction and apoptosis after myocardial ischemia and
reperfusion: Role of the terminal complement components and inhibition by
anti-C5 therapy.

AUTHOR: Vakeva Antti P; Agah Azin; Rollins Scott A; Matis Louis A; Li Lan;
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AUTHOR ADDRESS: (a)Cent. Exp. Ther. and Reperfusion Injury, Dep. Anesth.,
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JOURNAL: Circulation 97 (22):p2259-2267 June 9, 1998

ISSN: 0009-7322

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LANGUAGE: English

ABSTRACT: Background-Myocardial ischemia and reperfusion (MI/R)-induced
tissue injury involves necrosis and apoptosis. However, the precise
contribution of apoptosis to cell death, as well as the mechanism of
apoptosis induction, has not been delineated. In this study, we sought to
define the contribution of the activated terminal complement components
to apoptosis and necrosis in a rat model of MI/R injury. Methods and
Results-Monoclonal **antibodies** (mAbs; 18A and 16C) raised against
the rat C5 complement component bound to purified rat C5
(ELISA). 18A effectively blocked C5b-9-mediated cell lysis and C5a
-induced chemotaxis of rat polymorphonuclear leukocytes (PMNs), whereas
16C had no complement inhibitor activity. A single dose (20 mg/kg IV) of
18A blocked >80% of serum hemolytic activity for >4 hours. Administration
of 18A before myocardial ischemia (30 minutes) and reperfusion (4 hours)
significantly reduced (91%) left ventricular free wall PMN infiltration
compared with 16C treatment. Treatment with 18A 1 hour before ischemia or
5 minutes before reperfusion significantly reduced infarct size compared
with 16C treatment. A significant reduction in infarct size (42%) was
also observed in 18A-treated rats after 30 minutes of ischemia and 7 days
of reperfusion. DNA ladders and DNA labeling (eg, TUNEL assay)
demonstrated a dramatic reduction in MI/R-induced apoptosis in
18A-treated compared with 16C-treated rats. Conclusions-Anti-C5 therapy
in the setting of MI/R significantly inhibits cell apoptosis, necrosis,
and PMN infiltration in the rat despite C3 deposition. We conclude that
the terminal complement components C5a and C5b-9 are key mediators of
tissue injury in MI/R.

5/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11340383 BIOSIS NO.: 199800121715
Controlling the complement system in inflammation.
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305, 69120 Heidelberg**Germany
JOURNAL: Immunopharmacology 38 (1-2):p51-62 Dec., 1997
ISSN: 0162-3109
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Inappropriate or excessive activation of the complement system can lead to harmful, potentially life-threatening consequences due to severe inflammatory tissue destruction. These consequences are clinically manifested in various disorders, including septic shock, multiple organ failure and hyperacute graft rejection. Genetic complement deficiencies or complement depletion have been proven to be beneficial in reducing tissue injury in a number of animal models of severe complement-dependent inflammation. It is therefore believed that therapeutic inhibition of complement is likely to arrest the process of certain diseases. Attempts to efficiently inhibit complement include the application of endogenous soluble complement inhibitors (C1-inhibitor, recombinant soluble complement receptor 1-rsCR1), the administration of **antibodies**, either blocking key proteins of the cascade reaction (e.g. C3, C5), neutralizing the action of the complement-derived anaphylatoxin **C5a**, or interfering with complement receptor 3 (CR3, CD 18/11b)-mediated adhesion of inflammatory cells to the vascular endothelium. In addition, incorporation of membrane-bound complement regulators (DAF-CD55, MCP-CD46, CD59) has become possible by transfection of the correspondent cDNA into xenogeneic cells. Thereby, protection against complement-mediated inflammatory tissue damage could be achieved in various animal models of sepsis, myocardial as well as intestinal ischemia/reperfusion injury, adult respiratory distress syndrome, nephritis and graft rejection. Supported by results from first clinical trials, complement inhibition appears to be a suitable therapeutic approach to control inflammation. Current strategies to specifically inhibit complement in inflammation have been discussed at a recent meeting on the 'Immune Consequences of Trauma, Shock and Sepsis', held from March 4-8, 1997, in Munich, Germany. The Congress (chairman: E. Faist, Munich, Germany), which was held in close cooperation with various national and international shock and trauma societies, was attended by about 2000 delegates from 40 countries. The major objective of the meeting was to provide an overview on the most state-of-the-art methods to prevent multiple organ dysfunction syndrome (MODS)/multiple organ failure (MOF) following the systemic inflammatory response (SIRS) to severe trauma. One of the largest symposia held within the Congress was devoted to current aspects of controlling complement in inflammation (for abstracts see: Shock 1997, 7 Suppl., 71-75). After providing the audience with information on the scientific background by addressing the clinical relevance of complement activation (G.O. Till, Ann Arbor, MI, USA) and discussing recent developments in modern complement diagnosis (J. Kohl, Hannover, Germany), B.P. Morgan (Cardiff, UK) introduced the symposium's special issue by giving an overview on complement regulatory molecules. Selected topics included overviews on the application of C1 inhibitor (C.E. Hack, Amsterdam, NL), sCRI (U.S. Ryan, Needham, MA, USA),

antibodies to C5 (Y. Wang, New Haven CT, USA) and to the anaphylatoxin C5a (M. Oppermann, Gottingen, Germany), and a report on complement inhibition in cardiopulmonary bypass (T.E. Mollnes, Bodo, Norway). The growing interest of clinicians in complement-directed anti-inflammatory therapy, and the fact that only some of the various aspects of therapeutic complement inhibition could be addressed on the meeting, has motivated the author to expand a Congress report into a short comprehensive review on recent strategies to control complement in inflammation.

5/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10974348 BIOSIS NO.: 199799595493
Inhibition of complement activity by humanized anti-C5 antibody and
single-chain Fv.
AUTHOR: Thomas Thomas C(a); Rollins Scott A; Rother Russell P; Giannoni
Michelle A; Hartman Sandra L; Elliott Eileen A; Nye Steven H; Matis Louis
A; Squinto Stephen P; Evans Mark J
AUTHOR ADDRESS: (a)Alexion Pharmaceuticals, 25 Science Park, New Haven, CT
06511**USA
JOURNAL: Molecular Immunology 33 (17-18):p1389-1401 1996 (1997)
ISSN: 0161-5890
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Activation of the complement system contributes significantly to the pathogenesis of numerous acute and chronic diseases. Recently, a monoclonal **antibody** (5G1.1) that recognizes the human complement protein **C5**, has been shown to effectively block **C5** cleavage, thereby preventing the generation of the pro-inflammatory complement components **C5a** and C5b-9. Humanized 5G1.1 **antibody**, Fab and scFv molecules have been produced by grafting the complementarity determining regions of 5G1.1 on to human framework regions. Competitive ELISA analysis indicated that no framework changes were required in the humanized variable regions for retention of high affinity binding to C5, even at framework positions predicted by computer modeling to influence CDR canonical structure. The humanized Fab and scFv molecules blocked complement-mediated lysis of chicken erythrocytes and porcine aortic endothelial cells in a dose-dependent fashion, with complete complement inhibition occurring at a three-fold molar excess, relative to the human **C5** concentration. In contrast to a previously characterized anti-**C5** scFv molecule, the humanized h5G1.1 scFv also effectively blocked **C5a** generation. Finally, an intact humanized h5G1.1 **antibody** blocked human complement lytic activity at concentrations identical to the original murine monoclonal antibody. These results demonstrate that humanized h5G1.1 and its recombinant derivatives retain both the affinity and blocking functions of the murine 5G1.1 antibody, and suggest that these molecules may serve as potent inhibitors of complement-mediated pathology in human inflammatory diseases.

5/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10825740 BIOSIS NO.: 199799446885
Monoclonal **antibody** to **C5** inhibits **C5a** and C5b-9
generation without inhibition of C3 cleavage and significantly limits
myocardial ischemia and reperfusion induced tissue damage.
AUTHOR: Vakeva A(a); Rollins S A; Matis L A; Stahl G L
AUTHOR ADDRESS: (a)Brigham Women's Hosp., Boston, MA**USA
JOURNAL: Journal of the American College of Cardiology 29 (2 SUPPL. A):p
267A 1997
CONFERENCE/MEETING: 46th Annual Scientific Session of the American College
of Cardiology Anaheim, California, USA March 16-19, 1997
ISSN: 0735-1097
RECORD TYPE: Citation

LANGUAGE: English

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10514607 BIOSIS NO.: 199699135752

Amelioration of lupus-like autoimmune disease in NZB/W F-1 mice after treatment with a blocking monoclonal antibody specific for complement component C5.

AUTHOR: Wang Yi(a); Hu Qile; Madri Joseph A; Rollins Scott A; Chodera Amy; Matis Louis A

AUTHOR ADDRESS: (a)Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT 06511**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 93 (16):p8563-8568 1996

ISSN: 0027-8424

DOCUMENT TYPE: Article

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